

STIC Search Report Biotech-Chem Library

STIC Database Tracking Number: 137481

TO: David Lukton

Location: REM-3B75/3C70

Art Unit: 1653

Tuesday, November 16, 2004

Case Serial Number: 09/943002

From: Mary Jane Ruhl

Location: Biotech-Chem Library

Remsen 1-A-62

Phone: 571-272-2524

maryjane.ruhl@uspto.gov

Search Notes

Examiner Lukton,

Here are the results for your recent search request.

Please feel free to contact me if you have any questions about these results.

Thank you for using STIC services. We appreciate the opportunity to serve you.

Sincerely,

Mary Jane Ruhl Technical Information Specialist STIC Remsen 1-A-62 Ext. 22524



SEARCH REQUEST FORM (STIC)

Access DB#	
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Requestor's Name: David Lukton

Examiner number: 71263

Date: 11/9/04

Art Unit: 1653

Phone number: 571-272-0952

Serial Number:

09-943002

Mail Box: 3-C-70

Examiner Rm: 3-B-75

Results format: paper

* * * * * * * * * * * * *

<u>Title</u>: Novel reovirus-derived proteins and uses therefor

Applicant: Roy Duncan

Earliest Priority Date: 11/7/97

Please search SEQ ID NO: 14

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

November 15, 2004, 14:47:10 ; Search time 40 Seconds (without alignments) 232.113 Million cell updates/sec Run on:

US-09-943-002-14 720 Title: Perfect score:

1 MGQRHSIVQPPAPPPNAFVE......EENTRILNHDGRNPDGSINV 140 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Total number of hits satisfying chosen parameters: 478139 segs, 66318000 residues Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database:

/cgn2_6/ptodata/1/laa/5A_COMB.pep:*
/cgn2_6/ptodata/1/laa/5B_COMB.pep:*
/cgn2_6/ptodata/1/laa/6A_COMB.pep:*
/cgn2_6/ptodata/1/laa/6B_COMB.pep:*
/cgn2_6/ptodata/1/laa/PcTUS_COMB.pep:*
/cgn2_6/ptodata/1/laa/PcTUS_COMB.pep:* Issued Patents AA:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		*			SUMMARIES		
Result No.	Score	Query Match	Length	DB	ΙD	Description	
	85	11.8	159	4	US-09-248-796A-16594	Sequence 16594, A	
8	81	11.2	271	4	US-09-252-991A-21522	21522,	
m	80.5	11.2	415	4	US-09-710-279-1406		
4	80.5	11.2	458	m	US-09-134-001C-4663	4663,	
S	75.5	10.5	1220	~	US-08-843-530B-36	36, Ar	
9	75.5	10.5	1220	4	US-09-636-728-32	32,	
. 7	74	10.3	408	~	US-09-014-969-13	13,	
8	74	10.3	1726	4	US-09-700-227-2	2,	
0	74	10.3	1739	4	US-09-540-236-3739	Sequence 3739, Ap	
10	73	10.1	482	4	US-09-328-352-7784		
11	72.5	10.1	338	4	US-09-248-796A-26748	267	
, 12	72.5	10.1	751	~	US-08-843-530B-32	32	
13	72.5	10.1	751	4	US-09-636-728-29	29,	
14	71.5	9.9	1257	ო	US-08-611-729A-8	ω`	
15	71.5	6.6	1257	4	US-09-195-524-8		
16	17	6.6	174	4	US-09-134-000C-4758	47	
17	70	7.0	507	4	US-09-270-767-44005		
18	69	9.6	306	4	US-09-674-529B-2		
19	69	9.6	315	4	US-09-674-529B-6	ý	
	68	4.6	1014	4		807	
21	67	9.3	287	4	US-09-543-681A-5282	5282	
22	67	9.3	306	4	US-09-674-529B-4	4	
23	. 67	9.3	309	4	US-09-674-529B-12	12,	
24	67	9.3	315	4	US-09-674-529B-8	Seguence 8, Appli	
25	67	9.3	393	4	US-09-248-796A-18493	184	
56	67	9.3	266	4	US-09-543-681A-7802	Sequence 7802, Ap	
27	66.5	9.5	215	4	US-09-248-796A-23074	23074	

Sequence 21522, Application US/09252991A

Sequence 21522, Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION:

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF THE SEFERENCE: 107196.136

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

6839, Ap	12893, A	Appli	1046, A	.00, Ap	.26, Ap	3152, Ap	5598, Ap	, Appl	, Appl	Appli	Appli	Appli	.46, Ap	43662, A	6480, Ap	Appli	Appli
Sequence 68	Sequence 12	Sequence 4,	Sequence 59	Sequence 21	Sequence 31	Sequence 31	Sequence 55	Sequence 12,	Sequence 12	Sequence 4,	Sequence 8,	Sequence 3,	Sequence 11		Sequence 64	Sequence 4,	Sequence 4,
US-09-543-681A-6839	US-09-489-039A-12893	US-09-165-396-4	US-09-270-767-59046	US-09-540-236-2100	US-09-710-279-3126	US-09-710-279-3152	US-09-134-001C-5598	US-09-733-524A-12	US-09-092-315-12	US-09-142-551A-4	US-09-390-131-8	US-09-142-551A-3	US-09-538-092-1146	US-09-270-767-43662	US-09-134-000C-6480	US-09-529-279-4	US-10-158-895-4
4	4	4	4	4	4	4	m	4	m	m	4	ო	4	4	4	4	4
322	516	799	160	182	238	238	241	355	356	370	393	396	400	795	576	579	579
9.5	9.5	9.5	9.5	9.5	9.5	9.5	9.5	9.5	9.5	9.5	9.5	9.5	9.5	9.5	9.1	9.1	9.1
66.5	66.5	66.5	99	99	99	99	99	99	99	99	99	99	99	99	65.5	65.5	65.5
28	53	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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Sequence 16594, Application US/09248796A

Sequence 16594, Application US/09248796A

Patent No. 6747137

GENERAL INFORMATION:
FAPPLICATMT: Keith Weinstock et al

TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS

TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: NUMBER: US/09/248,796A

CURRENT FILING DATE: 1999-02-13

PRIOR APPLICATION NUMBER: US 60/074,725

PRIOR PAPLICATION NUMBER: US 60/074,725

PRIOR PRILING DATE: 1998-02-13

PRIOR PILING DATE: 1998-08-13

NUMBER OF SEQ ID NOS: 28208

SEQ ID NO 16594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         75 A-----GVASL------PLLNVIAHNPGSVISATPIYKGPCTGVPNSRLLQITSGTAREN 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            77 SONVHOGVARIQQQQQQQQQQQQQQQQQILGITISPEHDYVPPYTQTPNDN--DLGRFDKQGN 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18 FVEIVSSSTGIIIAVGIFAFIFSFL---YKLLOMYNRKSKNKKRKEQIREQIELGLLSYG 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61, Indels 20, Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
11.8%; Score 85; DB 4;
Best Local Similarity 28.6%; Pred. No. 0.071;
Matches 38; Conservative 14; Mismatches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  124 TRILNHDGRNPDG 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  135 FHLLN----RPEG 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; ORGANISM: Candida albicans
US-09-248-796A-16594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-252-991A-21522
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1 MGQRHSIVQPPAPPPNAFVEIVSSSTGIIIAVGIFAFIFSFLYKLLQWYNRKSKNKKRKE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2; Length 1220;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 458;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            33 GIFAFIFSFLYKLLOWYNRKSKNKKRKEQIREQIELGLLSYGAGV-ASLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 36, Application US/08843530B
Patent No. 5939306
GENERAL INFORMATION:
APPLICANT: Selitrennikoff, Claude
APPLICANT: Agnan, Jacqueline
APPLICANT: Alex, Lisa A.
APPLICANT: Simon, Melvin I.
TITLE OF INVENTION: Osmosenaing Histidine Kinases
NUMBER OF SEQUENCES: 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/843,530B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Medlen & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
11.2%; Score 80.5; DE
Best Local Similarity 34.0%; Pred. No. 1.1;
Matches 17; Conservative 13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10.5%; Score 75.5; I 23.3%; Pred No. 16; tive 22; Mismatches
         CURRENT APPLICATION NUMBER: US/09/134,001C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 16-APR-1997
CLASSIFICATION: 435
                                                                                         PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR PLILNG DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR PLING DATE: 1997-08-14
SEQ ID NOS: 5674
LENGTH: 458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-4663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INPORMATION:
NAME: MacKnight, Kamrin T.
REGISTRATION NUMBER: 38,230
REFERENCE/DOCKET NUMBER: UTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SS: not relevant
not relevant
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INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (415) 705-8410
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Matches 31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: San Francisco
STATE: California
COUNTRY: United Stat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-843-530B-36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-843-530B-36
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Patent No. 6380370
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: GTC-007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           81 BRAGLAGKKVLDIGC--GGGILSRAMAQRGANVTGIDMGEAPLAVARLHQLESGVAVDYR 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          73 YGAGVASLPLLNVIAHNPGSVISATPIYKGP-CTGVPN-----SRLLQITSGTAEENT 124
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Patent No. 6703492

GENERAL INFORMATION:
GENERAL INFORMATION:
MILLIAM JOHN

TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REPERENCE: PU3480US

CURRENT PELING DATE: 1000-11-09

PRIOR APPLICATION NUMBER: 60/164,258

PRIOR FILING DATE: 1999-11-09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11.2%; Score 81; DB 4; Length 271; 26.2%; Pred. No. 0.44; Live 25; Mismatches 53; Indels
PRIOR APPLICATION NUMBER: US 60/074,788 PRIOR PLIJNG DATE: 1998-02-18 PRIOR APPLICATION NUMBER: US 60/094,190 PRIOR FILING DATE: 1998-07-27 NUMBER PO SEQ ID NOS: 33142 SEQ ID NO 21522 LENGTH: 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        / OTHER INFORMATION: variable amino acid US-09-710-279-1406
                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-21522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity 26.2%
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SOPTWARE: Patentin Ver. 2.1
SEQ ID NO 1406
LENGTH: 415
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NAME/KEY: MOD_RES
LOCATION: (415)
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US-09-710-279-1406
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Best Local
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Matches
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QIREQIELGLLSYGAGVASLPLLNVIAHNPGSVISATPIYKGPCTG--VPNSRLLQITSG 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Seltrennikoff, Claude
APPLICANT: Seltrennikoff, Claude
APPLICANT: Pott, Greg
TITLE OF INVENTION: Hatidine Kinases of Aspergillus and Other Fungal
TITLE OF INVENTION: Species, Related Compositions, and Methods of Use
FILE REFERENCE: UTC-03758
CURRENT APPLICATION NUMBER: US/09/636,728
CURRENT FILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 08/843,530
PRIOR FILING DATE: 1997-04-16
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APPLICANT: Racie, Lisa A.
APPLICANT: Racie, Lisa A.
APPLICANT: Racie, David
APPLICANT: Teacy, Maurice
APPLICANT: Teacy, Michael J.
APPLICANT: Agostino, Michael J.
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
TITLE OF INVENTION SECRETED PROTEINS AND POLYNUCLEOTIDES
TITLE OF INVENTION SECRETED PROTEINS AND PROTEINS AND POLYNUCLEOTIDES
TITLE OF INVENTION SECRETED PROTEINS AND P
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23.3%; Pred. No. 16;
ttive 22; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                              Sequence 32, Application US/09636728
Patent No. 6716625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       , ORGANISM: Saccharomyces cerevisiae US-09-636-728-32
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; Sequence 13, Application US/09014969
; Patent No. 5965397
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McCoy, John M.
LaVallie, Edward R.
Racie, Lisa A.
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                           412 EAGSTTSVSGHGG 424
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                                                                                                                                          119 TABENTRILNHDG 131
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Best Local Similarity 23.33
Matches 31; Conservative
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ADDRESSEE: Genetics
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SOFTWARE: Patentin Ve.
SEQ ID NO 32
LENGTH: 1220
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APPLICANT:
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67 ELGL------LSYGAGVASLP-LLNVIAHN----PGSVISATPIYKGPCT- 105
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Patent No. 6706494

GENERAL INFORMATION:
APPLICANT: Ruelle, Jean-Louis
TITLE OF INVENTION: BASBO28 Polypeptides and Polynucleotides
TITLE OF INVENTION: Encoding Therefor From Moraxella Catarrhalis
TITLE OF INVENTION: Encoding Therefor From Moraxella Catarrhalis
TITLE OF INVENTION: Encoding Therefor From Moraxella Catarrhalis
CURRENT APPLICATION NUMBER: US/09/700,227

CURRENT FILING DATE: 1999-05-10

PRIOR PILING DATE: 1999-05-10

NUMBER OF SEQ ID NOS: 6

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 2

LEAVERMENT 1000

SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 GGGGDLHTPMLKLSYSTSQEFSSREELLSCKEEDKSQISFDNLTFSGTL 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          106 ---GVPNSRLLQITSGTA------EENTRILNHDGRNPDGSI 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 4; Length 1726;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2; Length 408;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                43; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63; Indels
SOFTWARE: PC-DOS/MS-DOS SOFTWARE: PACENTIN Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/014,969 FTLING DATE: CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               119 ----TAEENTRILNHDGR-----NPDGSINV 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10.3%; Score 74; DB 21.3%; Pred. No. 5.1; tive 32; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ch 10.3%; Score 74; DB 1 Similarity 23.5%; Pred. No. 39; 36; Conservative 24; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17 AFVELVSSSTGIIIAVGIFAFIFSFL-----
                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Sprunger, Suzanne A.
REGISTRATION NUMBER: 41,323
TELECOMMUNICATION INFORMATION:
TELEPRONE: (617) 496-8284
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPB: PRT ORGANISM: Moraxella catarrhalis
                                                                                                                                                                                                                                                                                                                                                                                                                              408 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 21.39
Matches 36, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: protein
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAL
TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
TITLE OF INVENTION: POR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: POR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/248, 796A
CURRENT FILING DATE: 1999-02-12
PRIOR FILING DATE: 1998-02-13
PRIOR FILING DATE: 1998-06-13
PRIOR PILING DATE: 1998-08-13
SEQ ID NOS: 28208
SEQ ID NOS: 28208
LENGTH: 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                34 IPAFIFSFLYKLLQWYNRKSKNKKRKEQ----IREQ------IBLGLLSYGAG 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                77 VASLPLINVIAHNPGSVI------SATPIYKGPCTGVPNSRLLQITSG 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 4; Length 338;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 32, Application US/08843530B
Patent No. 593306
GENERAL INFORMATION:
APPLICANT: Selitrennikoff, Claude
APPLICANT: Agnan, Jacqueline
APPLICANT: Alex, Lisa A.
TITLE OF INVENTION: Osmosensing Histidine Kinases
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSER: Medlen & Carroll, Lip
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/843,530B FILING DATE: 16-APP-1997 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Medlen & Carroll, LLP
STREET: 220 Montgomery Street, Sulte 2200
CITY: San Francisco
STATE: California
COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
10.1%; Score 72.5; DB
Best Local Similarity 22.8%; Pred. No. 5.8;
Matches 26; Conservative 17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIDLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: MacKnight, Kamrin T.
REGISTRATION NUMBER: 38,230
REFERENCE/DOCKET NUMBER: UTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INPORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 751 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                             Candida albicans
                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-248-796A-26748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JS-08-843-530B-32
                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM:
                                                                                                                     US-09-540-236-3739

Bequence 3739, Application US/09540236

Betent No. 6673910

GENERAL INFORMATION:

APPLICANT: Gary L. Breton et al.

TITLE OF INVENTION: NOCISIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATAR

TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 2709-2005-001

CURRENT APPLICATION NUMBER: US/09/540,236

CURRENT FILING DATE: 2000-04-04

NUMBER OF SEQ ID NOS: 3840

SEQ ID NO 3739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:

APPLICANT: Gary L. Brecon et al.

APPLICANT: Gary L. Brecon et al.

ITILE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER

TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS

FILE REPERENCE: GTC99-03PA

CURRENT APPLICATION NUMBER: US/09/328,352

CURRENT FILING DATE: 1999-06-04

NUMBER OF SEQ ID NOS: 8252

SEQ ID NO 7784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1494 SPIPVVGDIQGFVBAQTVGDHVFATIGLIPGLGDVAQKAHKAKKAYDTAKSANDVKGMKS 1553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 QIREQIELGLLSYGAGVASLPLLNVIAHNPGSVISATPIYKGPCTGVPNSRLLQITSG-- 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15 PNAF------VEIVSSSTGIIIAVGIFAFIFSFLYKLLQWYNRKSKNKKRKEQIR 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17 AFVEIVSSSTGIIIAVGIFAFIFSFL------YKLLQWYN-RKSKN--KKRKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     64 EQIBLGLLS-----YGAGVASLPLLNVIAHNPGSVISATPIYKGPCT 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20;
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10.1%; Score 73; DB 4; Length 482;
Best Local Similarity 30.6%; Pred. No. 8.4;
Matches 34; Conservative 13; Mismatches 38; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          43, Indels
1593 NIAGYTIDKNGRLHNNRGQFTSDPNNPRVSTNL 1625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                119 -----TABENTRILNHDGR-----NPDGSINV 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match

10.3*; Score '*; Local Similarity 23.5*; Pred. No. 39; Matches 36; Conservative 24; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 11
US-09-248-796A-26748
; Sequence 26748, Application US/09248796A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-328-352-7784
; Sequence 7784, Application US/09328352
; Patent No. 6562958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Acinetobacter baumannii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: PRT
; ORGANISM: M.catarrhalis
US-09-540-236-3739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |:| ::
1554 AIQEGVD---
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                        셤
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New York
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8
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                                                                                                                                                      280 PESLAKII---TGTVIAIGVPVILLTL--PLAHW------AVQPIVRLQKATELITEG 326
                                                                                                                                                                                                                 75 AGVASLPLLNVIAHNPGSVISATPIYKGPCTG--VPNSRLLQITSGTAEENTRILNHDGR 132
                                                                                                                                                                                                                                                        ----RASSFKRGFSSGFAVPSS-LLOPNTARAGSTTSVSGHGGS 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     280 PESLAKII---TGTVIAIGVPVILITL--PLAHW------AVQPIVRLQKATELITEG 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 75 AGVASLPLLNVIAHNPGSVISATPIYKGPCTG--VPNSRLLQITSGTAEENTRILNHDGR 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----RASSPKRGPSSGFAVPSS-LLQFNTABAGSTTSVSGHGGS 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15 PNAFVEIVSSSTGIIIAVGIFAFIFSFLYKLLQWYNRKSKNKKRKEQIREQIBLGLLSYG
                                                                                                                           15 PNAFVEIVSSSTGIIIAVGIFAFIFSFLYKLLQWYNRKSKNKKRKEQIREQIELGLLSYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Selftrennikoff, Claude
APPLICANT: Selftrennikoff, Claude
APPLICANT: Pott, Greg
TITLE OF INVENTION: Histidine Kinases of Aspargillus and Other Fungal
TITLE OF INVENTION: Species, Related Compositions, and Methods of Use
FILE REFERENCE: UTC-03758
CURRENT APPLICATION NUMBER: US/09/636,728
CURRENT PILING DATE: 2000-08-09
PRIOR APPLICATION NUMBER: 08/843,530
PRIOR APPLICATION NUMBER: 08/843,530
PRIOR APPLICATION NUMBER: 08/843,530
PRIOR FILING DATE: 1997-04-16
NUMBER OF SEQ ID NOS: 73
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 29
LENGTH: 751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               43; Indels 33; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
10.1%; Score 72.5; DB 4; Length 751;
Best Local Similarity 24.0%; Pred. No. 18;
Matches 31; Conservative 22; Mismatches 43; Indels 33
                                         Length 751;
                                                                                  Indela
                                      10.1%; Score 72.5; DB 2; 24.0%; Pred. No. 18;
                                                                               22; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Myat, Anna M.
Fleming, Robert J.
Artavanis-Tsakonas, Spyridon
Mann, Fobert S.
Gray, Grace E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ish-Horowicz, David
Henrique, Domingos M.P.
Lewis, Julian H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT; ORGANISM: Saccharomyces cerevisiae US-09-636-728-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 8, Application US/08611729A
Patent No. 6004924
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 29, Application US/09636728
Patent No. 6716625
                                                                                    31, Conservative
                                                                                                                                                                                                                                                          327 RGLS-----
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                                                                                                                                                                                                                                                                                                     133 -NPDGSINV 140
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                                      Query Match
Best Local Similarity
US-08-843-530B-32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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APPLICANT:
APPLICANT:
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                                                                                    Matches
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48 WYNRKSKNKKRKEQIREQIELGLLSYGAGVASLPLLNVIAHNPG-----SVISATPIY 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9.9%; Score 71.5; DB 3; Length 1257;
77.3%; Pred. No. 49;
Ve 18; Mismatches 63; Indels 31; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ...clicant: Gray, Grace E.
TITLE OF INVENTION: NUCLECTIDE AND PROTEIN SEQUENCES OF THE
TITLE OF INVENTION: NUCLECTIDE AND METHODS BASED THEREON
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennia ...
STREET
                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/611,729A
FILING DATE: 06-MAR-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mistrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/POCKET NUMBER: 7326-037
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         101 KGPCTGVPNSRLLQITSGTAEENTRILNHDGRNP 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: 18h-Horowicz, David
APPLICANT: Henrique, Domingos M.P.
APPLICANT: Lewis, Julian H.
APPLICANT: Myat, Anna M.
APPLICANT: Pleming, Robert J.
APPLICANT: Artavanis-Teakonas, Spyridon
APPLICANT: Mann, Robert S.
APPLICANT: Gray, Grace E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                        COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 8, Application US/09195524
; Patent No. 6703489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (212) 869-9741/8
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 1257 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 27.3%;
Matches 42; Conservative 1
                                       1155 Avenue of
                                                          CITY: New York
STATE: New York
COUNTY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New York
: U.S.A.
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Query Match
9.9%; Score 71.5; DB 4; Length 1257;
Best Local Similarity 27.3%; Pred. No. 49;
Matches 42; Conservative 18; Mismatches 63; Indels 31
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: EN PC compatible
OPERATIOR SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/195,524
FILING DATE:
CLASSIFICATION NUMBER: US/09/195,524
FILING DATE:
RILING DATE:
APPLICATION NUMBER: US/08/611,729
FILING DATE: O6-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: MISTOCK, S. Leelie
REGISTRATION NUMBER: 18,872
REFERENCE/COMMUTION:
TELLEPHONE: (212) 799-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 1257 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: unknown; MOLECULE TYPE: protein US-09-195-524-8
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48 WYNRKSKNKKRKEQIREQIELGLLSYGAGVASLPLLNVIAHNPG-----SVISATPIY 100 2 GORHSIVOPPAPPNAF-----VBIV---SSSTGIIIAV--GIFAFIFSFLYKLLO 47 : | | | : | | | 989 RRRCPGRPATR ----PSGRM-RRTRILAAVRRTP 1017 101 KGPCTGVPNSRLLQITSGTAEENTRILNHDGRNP 134 셤 δ È ઠે

31; Gaps

Search completed: November 15, 2004, 14:59:04 Job time: 42 secs

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November 15, 2004, 14:31:00 ; Search time 155 Seconds (without alignments) 324.014 Million cell updates/sec
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1 MGQRHSIVQPPAPPPNAFVE......EBNTRILNHDGRNPDGSINV 140
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5.1.6
Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                               2002273 segs, 358729299 residues
GenCore version
Copyright (c) 1993 - 2004
                                                                 OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                         Gapop 10.0 , Gapext 0.5
                                                                                                                                                                              US-09-943-002-14
                                                                                                                                                                                                                                                       BLOSUM62
                                                                                                                                                                                                                                                       Scoring table:
                                                                                                                                                                                                Perfect score:
                                                                                                                                                                                                                   Sequence:
                                                                                                                                                                                                                                                                                                             Searched:
                                                                                                       Run on:
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geneseqp2002s:* geneseqp2003as:* geneseqp2003bs:* A Geneseq 23Sep04:* geneseqp1980s:* geneseqp1990s:* geneseqp2000s:*geneseqp2001s:* geneseqp20048:*

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

seq length: 0 seq length: 200000000

Minimum DB & Maximum DB &

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Aay06113 Baboon re				Abm71462 Staphyloc	Ado25483 Saureus	ά,	Aag82156 S. epider		Abu42716 Protein e			Abb48477 Līsteria	Abu32700 Protein e		_	Abb93650 Herbicida	_	_	HTH	Abr41590 Human DIT	Staphy	4 C alut	표	Aay45161 Human sec
SUMMARIES	ΩI	AAY06113	AAU33910	AAU36895	ABU16411	ABM71462	AD025483	AB072776	AAG82156	ABU43432	ABU42716	ABP39818	AD025485	ABB48477	ABU32700	ABU26499	ABG13686	ABB93650	ADK61938	ADN07100	ADJ68848	ABR41590	ABM72920	AAG92924	AAW75856	AAY45161
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	Score	720	84	84	84	84	84	81	80.5	80.5	80.5	80.5	79	78	78	77.5	77	76.5	75.5	75.5	75	74.5	74.5	74.5	74	74
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1425 4 AAM80143 1726 3 AAY57572 1739 8 ADL06053 348 6 ADA48468 494 4 ABB61632 534 3 AAB01805 534 4 AAB31251 562 6 ADJ1472 482 6 ADJ1860 543 8 ADH71860 543 8 ADH71865 534 2 AAX26968 534 3 ADP76092 647 8 ADP76092 649 8 ADM48283 647 7 ADB64828	Aam80143 Human pro Aay57572 Moraxella Adl06053 M. catarr	Ada48468 Rice prot Abb61632 Drosophil Aay26967 Wheat Mlo	Aab11251 Amino aci Ab31251 Amino aci		Human Human	Aay26968 Wheat Mlo Aab31252 Amino aci Adn07097 S. cerevi	~-	Adb64828 Human pro Aab93302 Human pro
20000444440000000440000000000000000000	AAM80143 AAY57572 ADL06053	ADA48468 ABB61632 AAY26967	AAB01805 AAB31251 ABH31472	ADA36497 ADH71860	ABG96273 ADH71856	AAY26968 AAB31252 ADN07097	ADP76092 ADM48283	ADB64828 AAB93302
	55 26 39 8	248 346 346 540	4 4 C	325	9 20 20	4 4 6	19 8	37 7
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74 10.3 73.5 10.0 73.5 10.0 73.5 10.0 73.5 10.0 73.5 10.0 73.5 10.0 73.5 10.0 73.5 10.0 73.5 10.0 72.5 10.1 72.5 10.1 72.5 10.1 72.5 10.1	26 27 28	29 30 31	3 8 8	32	33	E 4 4	44 43	4 4 T

ALIGNMENTS

RESULT 1

Orthoreovirus; reovirus; BRV; P15 protein; fusogenic protein; cell fusion; membrane fusion; syncytium formation. 27. .41 /note= "transmembrane domain" Baboon reovirus fusogenic protein P15a. Location/Qualifiers AAY06113 standard; protein; 140 AA. 98WO-CA001046. 97US-00965708. (first entry) (UYDA-) UNIV DALHOUSIE. WPI; 1999-327410/27. N-PSDB; AAX58670. Baboon reovirus. WO9924582-A1. 06-NOV-1998; 17-NOV-1997; 16-AUG-1999 20-MAY-1999. AAY06113, Juncan R; Key Domain AAY06113

Fusogenic proteins from non-enveloped reoviruses.

Example 6; Page 53-54; 57pp; English.

The present sequence represents the fusogenic protein P15a of baboon recovirus (BRV). 2 Unrelated fusion proteins responsible for cell-cell fusion induced by avian recovirus (ARV) and the Only 2 fusogenic mammalian recoviruses, Nelson Bay virus (NBV) and BRV, are identified in this invention. These proteins are termed P11 for ARV and NBV (see also AAV66104, AAV66107 and AAV66110) and P15 for BRV. Fusogenic P11 and P15 are useful for (1) promoting fusion of cell, liposome or proteoliposome membranes; production of B and T cell hybridomas or other heterokaryons (they eliminate the need to use toxic chemicals such as PBG); (111) for producing fusions between liposomes and cells or other liposomes; and

themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi Klebsiella pneumoniae; coli, staphylococcus and Enerococcus faccalls. The invention is also useful for the identification of potential new targets for antibiotic consecution of potential new targets for antibiotic consecution in protein and to obscain contibiodies capable of binding to the expressed proteins. The proteins can entisense nucleic acid sequence is also useful to screen for homologous cucles acids which are required for cell proliferation in a wide variety of organisms. The present sequence represents an essential prokaryotic cellular proliferation protein. Note: The sequence data for this patent cid not form part of the printed specification, but was obtained in clacking trom wilpo at the printed specification, but was obtained in the will confirm and inequal protein sequences.

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use in the discovery of novel antibiotics, the essential genes

33 GIFAFIFSFLYKLLOWYNRKSKNKKRKROIRROIBLGLLSYGAGVASLPLLNVIAHNPGS 92

22; Gaps

ch 11.7%; Score 84; DB 4; Length 431; 1 Similarity 26.5%; Pred. No. 2.2; 26; Conservative 15; Mismatches 35; Indels

Query Match Best Local Matches

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(iv) for incorporation into liposomes to allow intra- or extracellular delivery of bioactive agents (e.g. nucleic acid, proteins and metabolic regulators), both in vivo and in cell cultures. Antibodies raised against Pil or Pis are useful for diagnosis and therapeutically (e.g. to block undestrable fusion processes). Pil and Pis are smaller than fusogenic proteins from enveloped viruses and are not glycosylated, so are essier to produce and purify using recombinant expression systems. They do not require a signal peptide for membrane entry, are not immunogenic and are functional at neutral ph
                                                                                                                                                                                                                                                                                                                                                                                                                                           QIREQIELGLLSYGAGVASLPLLNVIAHNPGSVISATPIYKGPCTGVPNSRLLQITSGTA 120
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                                                                                                                                                                                                                                                                Query Match 100.0%; Score 720; DB 2; Best Local Similarity 100.0%; Pred. No. 1.5e-72; Matches 140; Conservative 0; Mismatches 0;
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Antisense; prokaryotic cellular proliferation protein; antibiotic; antibacterial; drug design.
                                                       Staphylococcus aureus cellular proliferation protein #186.
      AAU33910 standard; protein; 431 AA
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27-NOV-2000; 2000US-0253625P.
22-DEC-2000; 2000US-0257931P.
16-FEB-2001; 2001US-0269308P.
                                                                                                                                                                          2000US-0206848P.
2000US-0207727P.
                                                                                                                                                  21-MAR-2001; 2001WO-US009180
                                                                                                                                                                 2000US-0191078P
                                        14-FEB-2002 (first entry)
                                                                                                Staphylococcus aureus
                                                                                                                 WO200170955-A2
                                                                                                                                                                  21-MAR-2000,
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26-MAY-2000;
                                                                                                                                 27-SEP-2001
                       AAU33910;
AAU33910
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Carr GJ;
                                                                                                  Antisense, prokaryotic cellular proliferation protein, antibiotic; antibacterial; drug design.
                                                                                                                                                                                                                                                                                                                                                                                  New polynucleotides for the identification and development of antibiotics, comprise sequences of antisense nucleic acids.
                                                                                                                                                                                                                                                                                                                      Trawick JD,
                                                                               Staphylococcus aureus cellular proliferation protein #1065.
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                                                                                                                                                                                                                                                                                                                                                                                                                  Example 3; SEQ ID NO 12488; 511pp; English
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                    AAU36895 standard; protein; 431
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2000US-0207727P.
2000US-0242578P.
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2001US-0269308P
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                                                            (first entry)
                                                                                                                                                                                                                                                                                                    (ELIT-) ELITRA PHARM INC.
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                                                                                                                                   Staphylococcus aureus.
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N-PSDB; AASS4754.
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                                                                                                                                                                                                                                     26-MAY-2000;
                                                                                                                                                                                                                                                                                                                       Haselbeck R,
Yamamoto RT,
                                                                                                                                                                                                                   21-MAR-2000;
                                                                                                                                                                                                                                                  23-OCT-2000;
                                                             14-FEB-2002
                                       AAU36895;
RESULT 3
          AAU36895
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The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes,

New polynucleotides for the identification and development antibiotics, comprise sequences of antisense nucleic acids.

Example 3, SEQ ID NO 5406; 511pp; English.

Trawick JD,

Wall D,

Zyskind JW,

Ohlsen KL, Xu HH;

Haselbeck R,

Yamamoto RT,

WPI; 2001-611495/70. N-PSDB; AAS51769.

(ELIT-) ELITRA PHARM INC

Claim 25; SEQ ID NO 44335; 1766pp; English.

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The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae, Pseudomonas acutisnosa and Enterococcus faccalls. The invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to identify cortes used in proliferation, to express these proteins. The proteins antisense nucleic acids can also discovery programmes. The used to screen compounds in rational drug discovery programmes. The bused to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence represents an essential prokaryotic cellular proliferation protein. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in clectronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----TPANIPPE 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    33 GIFAFIFSFLYKLLOWYNRKSKNKRKEQIREQIELGLLSYGAGVASLPLLNVIAHNPGS 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Antisense; prokaryotic essential gene; cell proliferation; drug design.
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Xu HH;
                                                                                                                                                                                                                                                                                                                                                                                                                                 22;
                                                                                                                                                                                                                                                                                                                                                                                          11.7%; Score 84; DB 4; Length 431; 26.5%; Pred. No. 2.2; ive 15; Mismatches 35; Indels
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Forsyth RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protein encoded by Prokaryotic essential gene #1938.
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Yamamoto R,
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Carr GJ,
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06-SEP-2001, 2001US-00948993.
25-OCT-2001, 2001US-0342923P.
08-FEB-2002, 2002US-0362699P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          194 IBSYVCKHLG-----
                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 26.5%
Matches 26, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Staphylococcus aureus.
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Trawick JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2003-029926/02.
N-PSDB; ACA20281.
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The invention relates to an isolated nucleic acid comprising any one of
the 6213 antisense sequences given in the specification where expression
the 6213 antisense sequences given in the specification where expression
the 6213 antisense sequences given in the specification where expression
the color acid (12) a host call containing the vector; (3) an isolated
acid, (2) a host call containing the vector; (3) an isolated
color acid; (4) an antibody capable of specifically binding
antisense nucleic acid; (4) an antibody capable of specifically binding
colliferation or the activity of a gene in an operon required for
proliferation or the activity of agene in an operon required for
colliferation or the activity of agene in an operon required for
colliferation or that has an activity against a biological pathway
required for proliferation, or that inhibits cellular proliferation; (8)
identifying a gene required for cellular proliferation or the biological
pathway in which a proliferation-required gene or its gene product lies
compound's activity; (11) a culture comprising strains in which the agene
compound's activity; (11) a culture comprising strains in which the content or underexpressed or underexpressed; (12) determining the extent
co which each of the strains is present in a culture or collection of
strains; or (13) identifying the target of a compound that inhibits the
colleration of an organism. The antisense nucleic acids required
context is contenting or secandidate molecules for rational
context is content or secandidate activity and activity of the extent of the collection of an organism or solution and collection of an organism. The antisense nucleic acids required
context is contenting the target candidate molecules for rational
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6; Length 431;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11.7%; Score 84; DB 6
ilarity 26.5%; Pred. No. 2.2;
Conservative 15; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Staphylococcus aureus protein #702.
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les 26; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 431 AA;
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Matches
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ABM71462
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(CHIR-) CHIRON SPA

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                                                                                                                 The invention relates to novel genes and encoded proteins from Staphylococcus aureus. A composition comprising the S. aureus protein, a nucleic acid encoding the protein, or an antibody to the protein, is useful as a pharmaceutical, particularly as a vaccine for treating or preventing infection due to Staphylococcus bacteria, specifically an infection caused by S. aureus. The composition is particularly useful for treating or preventing sepais in a patient. The composition can also be used for diagnostics. The protein is also used in an assay for enzymatic studies and as a target for antibiotics. This sequence represents one of the novel S. aureus proteins of the invention
                                                                                                                                                                                                                                                                                                             -----TFANIPPE 216
                                                        New Staphylococcus aureus protein, useful as a vaccine for treating or preventing Staphylococcal infection, specifically an infection caused by S. aureus, e.g. sepsis.
                                                                                                                                                                                                                                                                                          33 GIFAFIPSFLYKLLQWYNRKSKNKKRKEQIREQIELGLLSYGAGVASLPLLNVIAHNPGS 92
                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                       22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   antimicrobial, microbial disease, drug composition, vaccine, bacterial infection, antibacterial; food preservative.
                                                                                                                                                                                                                                                  11.7%; Score 84; DB 6; Length 454; 26.5%; Pred. No. 2.3;
                                                                                                                                                                                                                                                                      35; Indela
                                                                                                                                                                                                                                                                                                     93 VISATPIYKGPCTGVPNSRLLQITSGTAEENTRILNHD 130
                                                                                                                                                                                                                                                                                                                                             217 IBSYVCKHLG------IGTAPUSTQTLQRD 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                               S_aureus adenylosuccinate lyase purB protein Seq158.
                                                                                                                                                                                                                                                          Pred. No. 2.3;
                                                                                                Claim 1; SEQ ID NO 1404; 49pp; English.
         Scarselli M;
                                                                                                                                                                                                                                                                                                                                                                                                      ADO25483 standard; protein; 454 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2002US-0423759P.
2002US-0423758P.
2002US-0423791P.
2002US-0423832P.
2002US-0423875P.
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2002US-0424502P
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                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                            Best Local Similarity 26.5
Matches 26, Conservative
         Masignani V, Mora M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Staphylococcus aureus
                            WPI; 2003-120786/11.
                                      N-PSDB; ACF73022
                                                                                                                                                                                                                                Sequence 454 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO2004041854-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          06-NOV-2002; 2
07-NOV-2002; 2
07-NOV-2002; 2
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05-NOV-2002;
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05-NOV-2002;
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                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                  RESULT 6
ADO25483
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This invention relates to the identification of novel protein targets for the development of antimicrobial drugs against pathogenic bacteria.

C the development of antimicrobial drugs against pathogenic bacteria.

Specifically, it refers to recombinant proteins derived from the stappinococus aureus, Helicobacter pylori, Streptococcus pneumoniae, Staphylococus aureus, Helicobacter pylori, Streptococcus pneumoniae, Bacherichia coli, Enterococcus facealis or Pseudomonas aeruginosa. The present invention describes providing a three-dimensional structure for these crystallised proteins to identify a potential modulacor for the prevention or treatment of microbial diseases. Purthermore, contacting a prevention or treatment of microbial diseases. Purthermore, contacting a protein with a modulator can be useful for assaying protein activity and hence its viability in drug composition or vaccine. Accordingly, such compositions can be useful for treating protein activity and antibacterial agents useful as food preservatives or treating food antibacterial agents useful as food preservatives or treating food protein target of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacterial polypeptide composition useful for treating bacterial infection, has isolated, recombinant bacterial polypeptide such as GTP-binding protein Bra from Pseudomonas aeruginosa or adenylosuccinate lyase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     33 GIFAFIFSFLYKLLOWYNRKSKNKKRKEQIREQIELGLLSYGAGVASLPLLNVIAHNPGS 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Houston S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nethery K;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        93 VISATPIYKGPCTGVPNSRLLQITSGTAEENTRILNHD 130
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Ng I, Virag C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 41; SEQ ID NO 158; 566pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Vedadi M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dharamsi A, Vecaca.
                                                          2002US-0425118P.
2002US-0425126P.
2002US-0425162P.
                                                                                                                                                    003US-0453914P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           003US-0455010P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (AFFI-) AFFINIUM PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      from Enterococcus faecalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 26.5*
Matches 26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pinder B, A
Buzadzija K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2004-400642/37.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; ADO25482
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08-NOV-2002;
08-NOV-2002;
08-NOV-2002;
08-NOV-2002;
08-NOV-2002;
12-MAR-2003;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Edwards A, I
Mansoury K,
Mcdonald M,
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Staphylococcus epidermidis SR1 strain; infection; diagnosis; vaccination;

Staphylococcus epidermidis

endocarditis.

09-NOV-2000; 2000WO-US030782

17-MAY-2001

epidermidia open reading frame protein sequence SEQ ID NO:1406.

(first entry)

03-SEP-2001

AAG82156;

AAG82156 standard, protein, 415 AA

us-09-943-002-14.rag

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The invention relates to Pseudomonas aeruginosa polypeptides and the polymucleotides encoding them. The sequences are useful in diagnosis and therapy of pathological conditions, as molecular targets for diagnostics, prophylaxis and treatment of pathological conditions resulting from a bacterial infection, for evaluating a compound, such as a polypeptide, for the ability to bind a P. aeruginosa nucleic acid, as components of effective antibacterial targets, as templates for antibacterial drugs, including anti-P. aeruginosa drugs, as templates for recombinant production of P. aeruginosa-derived peptides or polypeptides, as target components for diagnosis and/or treatment of P. aeruginosa sequences or other sequence of Pseudomonas species using biochip technology. Sequences ABO67826-10 pequence data for this patent did not form part of the printed sequence that was obtained in electronic format from USPTO at sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel isolated nucleic acid encoding Peeudomonas aeruginosa polypeptide, useful as molecular targets for diagnostics, prophylaxis and treatment of pathological conditions resulting from bacterial infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13 PPPNAFVEIVSSSTGIIIAVGIFAFIFSFLYKLLQWYNRKSKNKKRKEQIREQIELGLLS 72
                                                                                                                                                                Bacterial infection; Pseudomonas aeruginosa infection; antibacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11.2%; Score 81; DB 7; Length 271; 26.2%; Pred. No. 2.6; ive 25; Mismatches 53; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                         Bush D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; SEQ ID NO 21522; 455pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                        Deloughery C,
                                                                                                                                  Pseudomonas aeruginosa polypeptide #4951.
                             AB072776 standard; protein; 271 AA.
                                                                                                                                                                                                                                                                                                                                                                                      (GENO-) GENOME THERAPEUTICS CORP.
                                                                                                                                                                                                                                                                                                                                    98US-0074788P.
                                                                                                                                                                                                                                                                                                    99US-00252991
                                                                                                                                                                                                                                                                                                                                                                                                                      Nolling J,
                                                                                                 (first entry)
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                                                                                                                                                                                                   Pseudomonas aeruginosa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2003-615309/58.
N-PSDB; ABD06347.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 271 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                      Rubenfield MJ,
                                                                                                                                                                                                                                US6551795-B1
                                                                                                                                                                                                                                                                                                    18-FEB-1999;
                                                                                                 29-JUL-2004
                                                                                                                                                                                                                                                                   22-APR-2003.
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Best Local Si
Matches 32,
                                                                AB072776;
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RESULT
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Nucleic acids encoding polypeptides from Staphylococcus epidermidis, useful for vaccinating against infections, e.g. endocarditis.

WPI; 2001-316495/33.

Kimmerly WJ;

N-PSDB; AAH53006

(GLAX) GLAXO GROUP

09-NOV-1999;

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(II), given in AAGB11454 to AAGB3120, from Staphylococcus epidermidis.

and (II) can have antibacterial activity and therefore can be used in vaccination. The nucleic acids (I) may be used to produce the S.

epidermidis polypeptides (II) via the production of vectors containing them which are used to produce hosts calls which express the colypeptides. The polypeptides (II) (and/or nucleic acids) may then be used to vaccinate subjects and to raise antibodies against the bacteria. The polypeptides may also be used to assay for other inhibitors of their activity and therefore identify compounds that may be used for the treatment of S. epidermidis infections, e.g. endocarditis. AAHS3971 to AAHS5090 represent specifically claimed S. epidermidis genomic DNA creatment oligonucleotide sequences and primers which are used in the exemplification of the present invention. N.B. The present invention sequence listing of the present specification, however the sequence sequence in the disclosure for SEQ ID NO:4465 to even though sequences are present in the continuation of the present specification, however the sequence in the disclosure for SEQ ID NO:4465 to even though sequences are present the present the present the sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAH52304 to AAH53970 represent nucleic acids (I) encoding polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gарв
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11.2%; Score 80.5; DB 34.0%; Pred. No. 5.2; tive 13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 18; Page 397-398; 2188pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABU43432 standard; protein; 431 AA.
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tes 17; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 415 AA;
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AC ABU4
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Antisense; prokaryotic essential gene; cell proliferation; drug design.
           Protein encoded by Prokaryotic essential gene #28959.
                                                                                 21-MAR-2001; 2001US-00815242.
06-SEP-2001; 2001US-00948993.
25-0CT-2001; 2001US-0342921P.
08-FEB-2002; 2002US-0072851.
06-MAR-2002; 2002US-0362699P.
                                                                      21-MAR-2002; 2002WO-US009107
                                   Staphylococcus haemolyticus
                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 34.0%
Matches 17; Conservative
19-JUN-2003 (first entry)
                                                                                                                      (BLIT-) ELITRA PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 431 AA;
                                               WO200277183-A2.
                                                          03-OCT-2002.
                                                                                                                                   ų,
                                                                                                                                   Wang |
8XCCCCCCCCCCCCCCCCCCCCCCCCCCCCCX
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the invention fractaces of an included and the following any own the invention where expression of the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid concluded are:

(2) a host cell containing the vector; (3) an isolated prolypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation or that has an activity against a biological pathway cequired for proliferation, or that inhibits cellular proliferation; (8) identifying a compound that influence the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound; a activity; (11) a culture compound that inhibits the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the gene proliferation of an organism. The antisense nucleic acids are quaired for cellular proliferation to solate candidate modeless or screening for homologous nucleic acids required for cellular proliferation to select conditions and activity of a selection of a compound that inhibits are lighted for cellular proliferation to solate candidate modeless or screening for homologous nucleic acids required for cellular proliferation to solate candidate modeless or screening for homologous nucleic acids required for cellular proliferation to solate the servent of the servent
                                                                                                                                                                                                                                                                                                                                              New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at fig. wipo.int/pub/published_pot_sequences
Zyskind JW;
Xu HH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     any
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         invention relates to an isolated nucleic acid comprising
Ohlsen KL,
Forsyth RA,
      Haselbeck R,
Yamamoto R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 25, SEQ ID NO 71356, 1766pp, English.
Malone C,
Carr GJ,
Zamudio C,
Trawick JD,
                                                                                                                                                                                WPI; 2003-029926/02
                                                                                                                                                                                                                                       N-PSDB; ACA47302
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the invention relates to an interact and where expression of the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid inhibits proliferation is inhibited by the antistense encoding a promoter operably linked to the nucleic acid.

(2) a vector comprising a promoter operably linked to the nucleic acid.

(3) a host cell containing the vector; (3) an isolated or nucleic acid; (2) a host cell containing the vector; (3) an isolated or nucleic acid; (4) an antibody capable of specifically binding the polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular compriseration; (7) identifying a gene in an operon required for proliferation or that has an activity against a biological pathway to the proliferation or that has an activity against a biological pathway in which a proliferation or the biological pathway in which a proliferation or the biological containing a gene required for cellular proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound; activity; (11) a culture comprising strains in which the test compound that inhibits the product is overexpressed or underexpressed; (12) determining the extent of the vertains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for proliferation are properties or screening for homologous nucleic acids are useful for drug discovery programs, or for screening homologous nucleic acids for this cepture or proliferation to isolate candidate model sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the present sequence is an organism.
                                                                                                                                The invention relates to an isolated nucleic acid comprising any
Claim 25; SEQ ID NO 70640; 1766pp; English
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19, Indels

11.2%; Score 80.5; DE 34.0%; Pred. No. 5.4; tive 13; Mismatches

DB 6; Length 431;

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antimicrobial; microbial disease; drug composition; vaccine;
bacterial infection; antibacterial; food preservative.
                                                                                                                                            S aureus adenylosuccinate lyase purB protein Seg160.
                   AD025485 standard; protein; 454 AA.
                                                                                                                                                                                                                                                                                                                                                                         05-NOV-2003; 2003WO-CA001671
                                                                                                                                                                                                                                                Staphylococcus aureus
                                                                                                                                                                                                                                                                                         WO2004041854-A2
                                                                                                                                                                                                                                                                                                                                                                                                                  05-NOV-2002;
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05-NOV-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-NOV-2002;
05-NOV-2002;
                                                                                                   12-AUG-2004
                                                            AD025485;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   36-NOV-2
  AD025485
                                                            ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABN90538 to ABN93374 represent Staphylococcus epidermidis open reading frame (ORF) nucleic acid sequences which encode the amino acid sequences given in ABP35124 to ABP37960. The S. epidermidis sequences have antibacterial activity and can be used in gene therapy. The sequences can also be used in the diagnosis and treatment of bacterial infections, particularly S. epidermidis infections. The sequences can be used to screen for compounds able to interfere with the S. epidermidis life cycle or inhibit S. epidermidis infection. N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the USPTO web site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Staphylococcus epidermidis; open reading frame; ORF; bacterial infection; antibacterial; gene therapy.
                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel isolated nucleic acid encoding a Staphylococcus epidermis polypeptide, useful for diagnosing and treating bacterial infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Staphylococcus epidermidis ORF amino acid sequence SEQ ID NO:4663.
                                                                                                                                            ä
                                                                                                                                                                                                           33 GIFAFIFSFLYKLLOWYNRKSKNKKRKEQIREQIELGLLSYGAGV-ASLP 81
                                                                                                     6; Length 431;
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                                                                                                                                        19; Indels
                                                                                                     8
                                                                                                   ; Score 80.5; Di
; Pred. No. 5.4;
13; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; SEQ ID NO 4663; 267pp; English.
in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (GENO-) GENOME THERAPEUTICS CORP.
                                                                                                                                                                                                                                                                                                                                ABP39818 standard, protein, 458
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34.0%;
                                                                                                   11.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Staphylococcus epidermidis.
                                                                             Query Match
Best Local Similarity 34...
--hes 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2002-381255/41
N-PSDB; ABN92363.
                                                            Sequence 431 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 458 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                  24-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13-AUG-1998;
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08-NOV-1997;
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                                                                                                                                                                                                                                                                                                                                                                         ÀBP39818;
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                                                                                                                                                                                                                                                                                       RESULT 11
ABP39818
XX ABP39
XX ABP39
XX ABP39
XX Staph
XX
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Bacterial polypeptide composition useful for treating bacterial infection, has isolated, recombinant bacterial polypeptide such as GTP-
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Alam MZ, Ng I, Virag C, Houston S;
                                                                                                                                                                                                                                                                                           US-0454193P
                                                                                                                                                                                                                                                                       003US-0454128P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Buzadzija K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dharamsi A,
                                                                                                                                                                                             US-042
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2004-400642/37.
N-PSDB; ADO25484.
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Mansoury K,
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Mcdonald M,
NOV
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Gaps

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19; Indels

Local Similarity 34.04

Matches

33 169

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RESULT 12

GIFAFIFSFLYKLLOWYNRKSKNKKRKEQIREQIELGLLSYGAGV-ASLP 81

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This invention relates to the identification of novel protein targets for the development of antimicrobial drugs against pathogenic bacteria. Specifically, it refers to recombinant proteins derived from Etaphylococcus aureus, Helicobacter pylori, Streptococcus preumoniae, Bacherichia coli, Enterococcus faecalis or Pseudomonas aeruginosa. The present invention describes providing a three-dimensional structure for these crystallised proteins to identify a potential modulator for the prevention or treatment of microbial diseases. Furthermore, contacting a protein with a modulator can be useful for assaying protein activity and hence its viability in drug composition or vaccime. Accordingly, such compositions can be useful for treating bacterial infections, developing antibacterial agents useful as food preservatives or treating food products to aliminate potential pathogens. This polypeptide sequence is a bacterial protein target of the invention.
protein Bra from Pseudomonas aeruginosa or adenylosuccinate lyase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----TFANIPPE 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             33 GIFAFIFSFLYKILQWYNRKSKNKKRKEQIREQIELGLLSYGAGVASLPLLNVIAHNPGS 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COBBART P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dussurget C, rrangeul L, Couve E, Rusnick C, Fsihi H, Dehoux F Dussurget O, Chetouani F, Nedjari H, Glaser P, Kunst F, Cossart Daniels J, Goebel W, Kreft J, Kuhn M, Ng B, Vazquez-Boland JA, Dominguez-Bernal G, Garrido-García P, Tierrez-Martinez A, Amend A, Chakraborty T, Domann E, Hain T, Berche P, Charbit A, Durant L, Perez-Diaz J, Baquero F, García Del Portillo F, Gomez-Lopez N; Raduenio B, De Pablos B, Wehland J, Kaerst U, Entian K. Hann F, Hann T, Berthe D, Butian K. Hann F, Hann T, Rose M, Voss H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Antibacterial; gene therapy; vaccine; biosynthesis; biodegradation; vitamin B12; bacterial infection; disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      22;
                                                                                                                                                                                                                                                                                                                                                                                                                  11.0%; Score 79; DB 8; Length 454; 25.5%; Pred. No. 8.6; ive 16; Mismatches 35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   93 VISATPIYKGPCTGVPNSRLLQITSGTAEENTRILNHD 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 41; SEQ ID NO 160; 566pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Listeria monocytogenes protein #1181,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABB48477 standard; protein; 391 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11-APR-2001; 2001WO-FR001118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11-APR-2000; 2000FR-00004629
                   from Enterococcus faecalis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        25; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                             Sequence 454 AA;
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Genomic sequence for Listeria monocytogenes, useful e.g. for treatment and prevention of Listeria and related bacterial infections, and related

WPI; 2002-010914/01.

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The present invention relates to the genome sequence of Listeria

monocytogenes EGD-e (see ABA3041). The genome sequence and fragments of

it are useful for selecting probes and primers for detecting genes in L.

concocytogenes and related organisms, and for studying genetic

monocytogenes and related organisms, and for studying genetic

polymorphisms and other genomes equence are useful for raising specific

expressed from the genome sequence are useful for raising specific

expressed from the genome sequence are useful for raising specific

antibodies, identification of L. monocytogenes and related organisms, and

for blooynthesis and biodegradation, especially biosynthesis of Vitamin

CC antibodies and biodegradation, especially biosynthesis of Vitamin

CC and modulate L. monocytogenes-related diseases. In addition, the genome

cs equence and proteins encoded by it are useful in pharmaceutical and

vaccines compositions for the treatment or prevention of infections by L.

CC monocytogenes and related organisms. Note: The sequence data for this

CD monocytogenes and related organisms. Note: The sequence data for this

CD in electronic format directly from WIPO at

CD monocytogenes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---LSYGAGVASLPLLNVIAHNPGS----VISATPIY 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  79 KKAAEESREQIEEALKGSDMVFVTAGMGGGTGTGAAPVIAQIAKEMGALTVGVVTRPFGF 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New antisense nucleic acids, useful for identifying proteins or screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Antisense; prokaryotic essential gene; cell proliferation; drug design.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              38; Gaps
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Xu HH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           101 KGP-----CTG------VPNSRLLQITSGTABENTRIL 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                        10.8%; Score 78; DB 5; Length 391; 28.3%; Pred. No. 9.1; ive 14; Mismatches 24; Indels
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Forsyth RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Protein encoded by Prokaryotic essential gene #18227.
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Yamamoto R,
                                                                                                                                                                                                                                                                                                                                                                                   ftp.wipo.int/pub/published_pct_sequences
                                  Claim 6; SEQ ID NO 1182, 192pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABU32700 standard; protein; 391 AA
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Carr GJ,
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06-SEP-2001; 2001US-00948993.
25-OCT-2001; 2001US-0342923P.
08-FEB-2002; 2002US-00072851.
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nes 30; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  56 KKRKEQIREQIELGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Listeria monocytogenes
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Trawick JD,
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                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 391 AA;
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polypeptides
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Wall D,
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Matches
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the invention transfer to an isolater in the invention where expression of the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated of polypeptide of its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting callular contisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting callular proliferation or the activity of a gene in an operon required for proliferation, (7) identifying a compound that influences the activity of required for proliferation, or that inhibits callular proliferation or the biological pathway contised for proliferation, or that inhibits proliferation or the biological pathway in which the test compound that inhibits proliferation or the biological pathway in which a proliferation required for cellular proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound; a activity; (11) a culture comprising strains in which the gene product is overexpressed or undersexpressed; (12) determining the extent of product is overexpressed or undersexpressed; (12) feremining the extent of compound; a activity; (11) a culture comprising strains in which the formalism. The antisense nucleic acids required for proliferation in cells other than S. arrens, S. typhimurium, confidentifying proteins or screening for homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, confident format directly from WIPO at the printed specification, but was obtained for the print of the printed specification, but we obtained for the printed specification, but which the properation of the printed specification, but which and a propera
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KKRKEQIREQIELGL-----LSYGAGVASLPLLINVIAHNPGS----VISATPIY 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Antisense; prokaryotic essential gene; cell proliferation; drug design.
                                                                                                                 an isolated nucleic acid comprising any one
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
  homologous nucleic acids required for cellular proliferation to
                     isolate candidate molecules for rational drug discovery programs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Protein encoded by Prokaryotic essential gene #12026.
                                                                   Claim 25; SEQ ID NO 60624; 1766pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ftp.wipo.int/pub/published_pct_sequences
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Matches 30; Conservative
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21-MAR-2001, 2001US-00815242

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The invention relates to an isolated nucleic acid comprising any one of the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid nucleic acid (2) a host cell concaining the vector; (3) an isolated conceding a polypeptide whose expression is inhibited by the antisense conclude acid; (4) an antibody capable of specifically binding antisense nucleic acid; (4) an antibody capable of specifically binding colliferation or the activity of a gene in an operon required for proliferation or the activity of a gene in an operon required for proliferation, (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or the biological corresponds in antibody as activity; (11) a culture compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the extent or owhich each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for collecting or collection of correcting the capacity and collection of correction or strains or screening for homologous nucleic acids are useful for collection of correction or sollection or sequence or is solate encleanced.
                                                                                                                                                                                                                                                                                                                   New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 WILDKEKNIILQNQEALKNPKLLSIISLDKIRDELBFBGRFYA------VKIIAHNBK 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          48 WYNRKSKN-----KKRK-----EQIREQIELGLLSYGAGVASLPLLINVIAHNPG 91
                                                                                                                                                             Zyskind JW;
Xu HH;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              92 SVISATPIYKGPCTGVPNSRLLQITSGTABENTRILNHDGRNPDGSINV 140
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                                                                                                                                                                  Ohlsen KL,
Forsyth RA,
                                                                                                                                                                  Haselbeck R,
Yamamoto R,
                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 25; SEQ ID NO 54423; 1766pp; English.
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                                                                                                                                                                  Malone C,
                                                                                                                                                                                            Carr GJ,
                  25-OCT-2001; 2001US-0342923P.
08-FEB-2002; 2002US-00072851.
06-MAR-2002; 2002US-0362699P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31; Conservative
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Trawick JD,
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Wall D,
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Sequence 45755, A
Sequence 8926, Ap
Sequence 70640, A
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Sequence 5406, Ap
Sequence 12488, A
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351.310 Million cell updates/sec
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/ cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
/ cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
/ cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
/ cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
/ cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
/ cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
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/cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
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GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
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US-09-815-242-5406
US-09-815-242-12488
US-10-281-122A-44335
US-10-282-124-45755
US-10-739-930-8926
US-10-282-122A-71356
US-10-282-12A-71356
US-10-424-599-200688
US-10-424-144-39701
US-10-425-114-43526
US-10-425-114-43526
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                                                                                                                               November 15, 2004, 14:51:55
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Maximum Match 100%
Listing first 45 summaries
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                                                                                       OM protein - protein search, using sw model
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Maximum DB seq length: 200000000
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Match Length DB
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14 78 10.8 325 14 US-10-369-493-10884 16 77.5 10.8 391 15 US-10-282-122A-60624 17 77.5 10.8 606 15 US-10-452-114-54423 19 77.5 10.8 606 14 US-10-36-33-2 20 75.5 10.5 1220 9 US-09-493-5059 21 75.5 10.4 601 16 US-10-36-493-2082 22 75 10.4 601 16 US-10-437-963-149924 23 74.5 10.3 498 9 US-10-437-963-149924 24 74.5 10.3 498 9 US-10-425-114-5399 25 74.5 10.3 498 9 US-10-425-114-5399 26 74.5 10.3 498 9 US-10-425-114-5399 27 73 10.1 468 1 US-10-425-114-5399 28 73 10.1 26 10.2 US-10-425-11	0	e TORR	Sequence 60624,	Sequence 54423,	Sequence 54999,	Sequence 5059,	Sequence 332, Ag	Sequence 22082,	Sequence 149924	Sequence 654, 1	Sequence 53999,	Sequence 6678, 2	Sequence 150408	Sequence 4998,	Sequence 59396,	equen	Sequence 302682,	Sequence 312699	Sequence 51670,	equen	Sequence 274608	Sequence 701, A	Sequence 2982,	Sequence 190899	Sequence 160666	Sequence 52165,	Sequence 3051,	equen	Sequence 8, Apr	584	e 1258	e 1422	Sequence 9, Appl:	
78 10.8 325 1 77.5 10.8 325 1 77.5 10.8 391 1 77.5 10.8 654 1 77.5 10.8 654 1 77.5 10.8 654 1 77.5 10.8 654 1 77.5 10.8 654 1 77.5 10.8 654 1 77.5 10.8 654 1 77.5 10.1 649 1 77.5 10.1 649 1 72 10.1 766 1 72 10.1 766 1 72 10.0 649 1 72 10.0 649 1 72 10.0 649 1 72 10.0 649 1 72 10.0 649 1 72 1 72 10.0 649 1 72 1 72 10.0 649 1 72 1 72 1 72 1 72 1 72 1 72 1 72 1 7		-10-369-493-10884	282-122A-6062	282-122A-5442	425-114-5499	369-493-505	101-368-33	369-493-2208	437-963-14992	408-765A-65	425-114-5399	38-626-	424-599-15040	369-493-499	282-122A-5939	425-114-4148	425-115-30268	425-115-31269	425-114-5167	471-449-11	425-115-27460	310-154-7	104-047-2	425-115-19089	437-963-16066	282-122A-5216	320-797-305	369-493-2077	US-10-487-421-8	437-963-15843	437-963-12581	437-963-14223	-10-195-144-	
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ALIGNMENTS

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61 QIREQIELGILISYGAGVASLPLINVIAHNPGSVISATPIYKGPCTGVPNSRLLQITSGTA 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gape
                                                                                                  APPLICANT: Duncan, Roy
TITLE OF INVENTION: NOVEL REOVIRUS-DERIVED PROTEINS AND USES THEREFOR
FILE REFERENCE: 78973-1C
CURRENT APPLICATION NUMBER: US/09/943,002
CURRENT FILING DATE: 2001-08-31
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PSECSEQ for Windows Version 3.0
SEQ ID NO 14
LENGTH: 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
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                Sequence 14, Application US/09943002
Patent No. US20020045734A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT

ORGANISM: baboon reovirus
US-09-943-002-14
-09-943-002-14
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33 GIFAFIFSFLYKLLOWYNRKSKNKKRKEQIREQIELGLLSYGAGVASLPLLNVIAHNPGS 92
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 9; Length 431;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      35; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ch 11.7%; Score 84; DB 9
1 Similarity 26.5%; Pred. No. 2.1;
26; Conservative 15; Mismatches
                 PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-110-23
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-12-25
PRIOR PRIOR DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FREESEQ FOR WINDOWS VERSION 4.0
SOFTWARE: FREESEQ FOR WINDOWS VERSION 4.0
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CURRENT APPLICATION NUMBER: US/10/282,122A

CURRENT PILING DATE: 2003-02-20

PRIOR APPLICATION NUMBER: 60/191,076

PRIOR PILING DATE: 2000-03-21

PRIOR PILING DATE: 2000-05-23

PRIOR PILING DATE: 2000-05-26

PRIOR PILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR APPLICATION NUMBER: 60/207,327

PRIOR APPLICATION NUMBER: 60/230,335

PRIOR PILING DATE: 2000-09-09

PRIOR PILING DATE: 2000-09-09

PRIOR PILING DATE: 2000-09-09

PRIOR PILING DATE: 2000-09-09

PRIOR APPLICATION NUMBER: 60/242,578

PRIOR PILING DATE: 2000-10-23

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Publication No. US20040029129A1
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                                                                                                                                                                                                                                                                                                                                                                                                                      i TYPE: PRTj ORGANISM: Staphylococcus aureusUS-09-815-242-12488
2000-05-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Yamamoto, Robert
Forsyth, R.
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Best Local S
Matches 26
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                                                                                                                                                                                                         APPLICANT: Trail, Daniel

APPLICANT: Trail, John D.

APPLICANT: Trail, John D.

APPLICANT: Carr, Grant J.

APPLICANT: Carr, Grant J.

APPLICANT: Carr, Grant J.

APPLICANT: Xu, H. Howard

TITLE OF INVENTION: Identification of Essential Genes in

TITLE OF INVENTION: Prokaryctes

TITLE OF INVENTION: DATE: 2001-03-21

PRIOR APPLICATION NUMBER: 60/191, 078

PRIOR PILLING DATE: 2000-05-26

PRIOR PILLING DATE: 2000-05-26

PRIOR PILLING DATE: 2000-10-23

PRIOR PILLING DATE: 2000-11-27

PRIOR PILLING DATE: 2000-11-27

PRIOR PILLING DATE: 2000-11-22

PRIOR PILLING DATE: 2000-11-22

PRIOR PILLING DATE: 2000-11-22

PRIOR PILLING DATE: 2000-11-22

PRIOR PILLING DATE: 2001-12-22

PRIOR PILLING DATE: 2001-12-12

PRIOR PILLING DATE: 2001-12-12

PRIOR PILLING DATE: 2001-12-12

PRIOR PILLING DATE: 2001-12-12

PRIOR PILLING DATE: 2001-110

SOOTWARE: PRESEQ FOR Windows Version 4.0
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APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
RPPLICANT: Xu, H. Howard: T.
ITLE OF INVENTION: Identification of Essential Genes in ITLE OF INVENTION: Prokaryotes
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CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
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Patent No. US20020061569A1
                          Sequence 5406, Application US/09815242
Patent No. US20020061569A1
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CATION NUMBER: 60/191,078
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US-09-815-242-5406
                                                                                                                                         Ohlsen, Kari L.
Zyskind, Judith W.
Wall, Daniel
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Zyskind, Judith W.
Wall, Daniel
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22; Gaps

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TYPE: PRT
ORGANISM: Glycine max
FEATURE:
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CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
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TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
TITLE OF INVENTION: PLANTS AND USES THEREOF FOR PLANT IMPROVEMENT
FILE REFERENCE: 38-21 (53377) B
                                                                                                                                                                                                                                                                                                                                                                                                 142 GVHAEPTTFGVKMALMYTEMQRNLQRPKQVREEIEVGKMSGAVG-----TFANIPPE 193
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                                                                                                                                                                                                                                                                                                                                                  33 GIFAFIPSFLYKLLQWYNRKSKNKKRKEQIREQIELGLLSYGAGVASLPLLNVIAHNPGS 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5 HSIVQPPAPPPNA------FVEIVSSSTGIIIAVGIFAFIFSFLYKLLQWYN 50
                                                                                                                                                                                                                                                                                              Gaps
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Remaining Prior Application data removed - See File Wrapper or PALM. NUMBER OF SEQ 1D NOS: 78614
SOFTWARE: Patentin version 3.1
SEQ 1D NO 44335
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                                                                                                                                                                                                                                       ; Score 84; DB 15; Length 431;
; Pred. No. 2.1;
15; Mismatches 35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11.7%; Score 84; DB 15; Length 636; 22.0%; Pred. No. 3.5; tive 26; Mismatches 64; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           , OTHER INFORMATION: Clone ID: 700834446_FLI.pep
US-10-425-114-45755
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Publication No. US20040034888A1
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                                                                                                                           TYPE: PRT CAGANISM: Staphylococcus aureus US-10-282-122A-44335
                                                                                                                                                                                                                                    Query Match
Best Local Similarity 26.5%;
Matches 26; Conservative 15
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Best Local Similarity 22.04
Matches 35; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Glycine max
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LENGTH: 636
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280 ÓPPSPPPPPAAVVPKESKSSNKVGVIVGSVLGGFAFLVLLSLLVLWLLKYKOKKKIQOME 339
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                                                                                                                                                                                                         ; OTHER INFORMATION: Clone ID: GLVMA-23APR03-C245578_1.p
US-10-739-930-8926
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CURRENT APPLICATION NUMBER: US/10/739,930
CURRENT FILING DATE: 2003-12-18
NUMBER OF SEQ ID NOS: 11088
SEGO ID NO 8926
LENGTH: 376
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Publication No. US20040029129A1
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PRIOR FILING DATE: 2000-11-27
PRIOR PELING DATE: 2000-11-27
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-09
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PRIOR APPLICATION WUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-06
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-09-09
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ORGANISM: Staphylococcus epidermidis
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PRIOR APPLICATION NUMBER: 60/191,078
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Malone, Cheryl
Haselbeck, Robert
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Yamamoto, Robert
Forsyth, R.
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Best Local Similarity 29.7
Matches 22; Conservative
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Trawick, Joh
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TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REPERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT PILING DATE: 2000-03-02-03
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,335
PRIOR PILING DATE: 2000-09-06
PRIOR PILING DATE: 2000-09-09
PRIOR PILING DATE: 2000-09-09
PRIOR PILING DATE: 2000-09-09
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-11-27
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                                                                                                                   142 GVHAEPTTFGVKMALMYTEMKRNLKRPKEVRKEIEVGKMSGAVGTFANIP 191
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Length 431;
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                                                            Indels
      DB 15;
Ouery Match
11.2%; Score 80.5; DE
Best Local Similarity 34.0%; Pred. No. 5.1;
Matches 17; Conservative 13; Mismatches
                                                                                                                                                                                                                                                                                                                                Sequence 71356, Application US/10282122A Publication No. US20040029129A1 GENERAL INFORMATION:
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; Sequence 200688, Application US/10424599
; Publication No. US20040031072A1
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APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Hagelbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
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Carr, Grant
Yamamoto, Robert
Forsyth, R.
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APPLICANT: Lau, Jingdong
APPLICANT: Kovalic, David K.
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Gao, Yongwei
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE OF INVENTION: 1003-04-28
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NOS: 73128
TYPE. DESTRUCTOR OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            58 RKEQIREQIELGILSYGAGVASLPLLNVIAHNPGSVI------SATPIYKGPC 104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9 OPPAPPPNAFVEIVSS-----STGIIIAVGI-FAFIPSFLYKLLOWYNRKSKNKK 57
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APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 30 21(53223) B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
LENGTH: 756
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US-10-424-599-200688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
11.2%; Score 80.5; DB 15;
Best Local Similarity 25.7%; Pred. No. 11;
Matches 38; Conservative 18; Mismatches 45;
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US-10-425-114-39701
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MU, Wei Metabalk, Brad A. Applicant: Boukharov, Andrey A. APPLICANT: Barbazuk, Brad APPLICANT: Barbazuk, Brad APPLICANT: Barbazuk, Brad APPLICANT: Li, Ping TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REPERENCE: 38-21(5321)8 CURRENT PLILING DATE: 2003-05-14 NUMBER OF SEQ ID NOS: 204966 SEQ ID NOS: 204966 SEQ ID NO 183058 SEQ ID NO 183058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               239 PPPIAHLHAVKA------IMEMLWWYNNGYKVKMESERSNQGIMEEDSV 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  71 LSYGAGVASLPLLNVIAHNPGSVISATPIYKGPCTGVPNSRLLQI------TSGTAEEN 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13 PPPNAFVEIVSSSTGIIIAVGIFAFIFSFLYKLLQWYNRKSKNKKRKEQIREQI---ELGL
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US-10-437-963-183058
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10.9%; Score 78.5; DB 16;
Best Local Similarity 23.0%; Pred. No. 8.3;
Matches 32; Conservative 22; Mismatches 44;
Sequence 183058, Application US/10437963 Publication No. US20040123343A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               124 TRIL-----NHDGRNPDG 136
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ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-369-493-10884
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                                                                                                                                                  Sequence 290480, Application US/10425115
Publication No. US20040214272A1
Publication No. US20040214272A1
Publication No. US20040214272A1
APPLICANT: La Rosa; Thomas J.
APPLICANT: La Rosa; Thomas J.
APPLICANT: Cao, Yongwai
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants
FILE REPERENCE: 38-21 (5322) B4
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 29480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Staven B
APPLICANT: Craen, Staven B
APPLICANT: Cao, Yongwel
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERENCE: 38-21(53313)8
CURRENT APPLICATION NUMBER: US/10/425,114
. UNDER OF SEC ID NOS: 73128
SEC ID NO 4326
LENGTH: 544
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11.0%; Score 79.5; DB 17; Length 539; 35.6%; Pred. No. 8.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: Clone ID: MRT4577_28005C.1.pep
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US-10-425-114-43526
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                             389 EPGGVSSSRSWFTYEELIQATNGPSAQN 416
    --- LLQITSGTAEEN 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21; Conservative
  105 T--GVPNSR-
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Best Local Similarity
Matches 21; Conserv
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US-10-425-114-43526
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41;

Indels

Length 419;

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APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Blater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Ghen, Xianfeng
TITLE OF INVENTION: EXRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: EXPERSION OF MICROBIAL PROPERTIES
FILE REFERENCE: 30-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT PILING DATE: 2002-02-28
PRIOR FILING: DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
LENGTH: 325
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
) ORGANISM: Sphingomonas aromaticivorans
US-10-369-493-10884
Sequence 10884, Application US/10369493
Publication No. US20030233675A1
GENERAL INFORMATION:
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RESULT 13 US-10-437-963-183058

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56 KKRKEQIREQIELGL-----LSYGAGVASLPLLNVIAHNPGS----VISATPIY 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Identification of Essential Genes in Microorganisms FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-00
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-03-21
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; Pred. No. 8.6;
14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: 60/151,0/8
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR PILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR PILING DATE: 2000-09-06
PRIOR FILING DATE: 2000-09-06
PRIOR FILING DATE: 2000-09-09
PRIOR FILING DATE: 2000-10-29
PRIOR FILING DATE: 2000-10-29
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-110-27
PRIOR PILING DATE: 2000-110-27
PRIOR PRILING DATE: 2000-110-27
PRIOR PRILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-09
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PRIOR FILING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
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Sequence 60624, Application US/10282122A Publication No. US20040029129A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 10.8
Best Local Similarity 28.3
Matches 30; Conservative
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tryptophan-tRNA li adenylosuccinate l	hypothetical prote probable transcrip	lipase A precursor	hypothetical prote	hypothetical prote phosphoribosylamin	hypothetical prote hypothetical prote	periplasmic sugar-	cycochrome F450 ZD conserved hypothet	PTS system, mannit	phosphotransferase
AH3477 A72294	B83931 T38660	S61927	D96711	F71110 S60392	T33810 T32074	AH1934	AD0691	E95045	D97916
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385	445	323	708	358 557	881 1119	432	200	583	583
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71.5 9.9	70.5 9.8	70 9.7	70 9.7	69.5 9.7	69.5 9.7 69.5 9.7	9.6	69 9.6	9.6 69	9.6

ALIGNMENTS

RESULT 1
C89979
adenylosuccinate lyase [imported] - Staphylococcus aureus (strain N315) C:Species: Staphylococcus aureus
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004 C:Accession: C89979
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kalto, C.; Sekimizu, K.; C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001 A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus. A;Reference number: A89758, MUID:21311952; PMID:11418146
A,Accession: C89979 A,Status: preliminary A,Molecule type: DNA
A, Residues: 1-431 < KUR> A, Cross-references: UNIFOT: Q995X9; GB:BA000018; PID:g13701701; PIDN:BAB42994.1; GSPDB: A. Experimental source: strain N115
C;Genetics: A;Gene: purB C;Superfamily: fumarate hydratase
Query Match Best Local Similarity 26.5%; Pred. No. 1.8; Matches 26; Conservative 15; Mismatches 35; Indels 22; Gaps 2;
QY 33 GIPAPIFSFLYKLLQWYNRKSKONKRKEQIREQILEGLGSYGAGVASLPLLINVIAHNPGS 92
=
QY 93 VISATPIYKGPCTGVPNSRLLQITSGTABENTRILAHD 130
Db 194 iBSYVCKHLGIGTAPVSTQFLQRD 217
RESULT 2 phosphoribosylaminoimidazole carboxylase (BC 4.1.1.21) catalytic chain - Aquifex aeolics cypeises: Aquifex aeolicus cypeises: Aquifex aeolicus cybate: 08-May-1998 #text_change 09-Jul-2004 cybate: 08-May-1998 #text_change 09-Jul-2004 cybacession: D70401 R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.B.; Or Nature 392, 353-358, 1998 A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus. A;Reference number: A70300; MUID:98196666; PMID:9537320 A;Reference number: A70300; MUID:98196666; PMID:9537320 A;Reference number: D70401 A;Reference number: A70300; MUID:98196666; PMID:9537320 A;Reference number: A70400 A;Reference number: A70400 A;Reference number: B70401 A;Reference

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A;Accession: AH1699
A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Ccoss-references: UNIPROT:Q929Y5; GB:AL592022; PIDN:CAC97368.1; PID:g16414652; GSPDB:CA;Experimental source: strain Clip11262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Listeria innocus
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C;Accession: AH1699
R;Glacer, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecke:
.; Dominguez-Bernal, G.; Duchaud, B.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H
D; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Mattournam, A.; M.
A;Authors: Kreft, J.; Kuhn, M.; Taterra, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland.
A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cell-division initiation protein Ft8Z homolog ft8Z [imported] - Listeria innocua (strai)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  signal transduction histidine kinase Cj0793 [imported] - Campylobacter jejuni (strain N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; Species: Campylobacter jejuni
C; Date: 11-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C; Accession: A31351
R; Parkhill, J; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chillii
C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barre.
Nature 403, 665-668, 2000
A; Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyman A; Reference number: A81250; WUID:20150912; PMID:10688204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A,Cross-references: UNIPROT:Q3PPC6, GB:AL139076, GB:AL111168, NID:g6968128, PIDN:CAB7309. A,Experimental source: serotype O2, strain NCTC 11168
A;Cross-references: UNIPROT:Q8Y5M5; GB:NC_003210; PIDN:CAD00110.1; PID:g16411502; GSPDB
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                                                                                                                                                                                                                                                                                                                                    56 KKRKEQIREQIELGL-----LSYGAGVASLPLLNVIAHNPGS----VISATPIY 100
                                                                                                                                                                                                                                                                                                                                                                                                      79 KKAAEESREQIEEALKGSDMVFVTAGMGGGTGTGAAPVIAQIAKEMGALTVGVVTRPFGF 138
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                                                                                                                                                                                                                                                                     38; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         101 KGP-----CTG-------VPNSRLLQITSGTAEENTRIL 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                101 KGP-----CTG-------VPNSRLLQITSGTABENTRIL 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10.8%; Score 78; DB 2; Length 392; 28.3%; Pred. No. 6.4; ive 14; Mismatches 24; Indels
                                                                                                                                                                                                   DB 2; Length 391;
                                                                                                                                                                                               Query Match
10.8%; Score 78; DB 2; Length 391
Best Local Similarity 28.3%; Pred. No. 6.3;
Matches 30; Conservative 14; Mismatches 24; Indels
                                  A;Experimental source: strain EGD-e
C,Genetics:
A;Gene: ftsz
C;Superfamily: cell division protein ftsz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A,Gene: ftsZ
C,Superfamily: cell division protein ftsZ
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Matches 30, Conservative
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A; Residues: 1-339 < PAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A, Status: preliminary
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Molecule type: DNA
Residues: 1-255 <WHI>
Cross references: UNIPROT: Q9RWX1; GB: AE001912; GB: AE000513; NID: 96458228; PIDN: AAF1011
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Ridlaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker, Dominguez-Bernal, G.; Duchaud, B.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H. D.; Jones, L.M.; Karat, G.; Duchaud, B.; Rurand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H. Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kunh, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Mahand, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CjAccession: A75507
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma
S.; Mith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A;Reference number: A75250; MUID:20036896; PMID:10567266
                               A/Gene: purB
C;Superfamily: phosphoribosylaminoimidazole carboxylase catalytic chain; phosphoribosyls
C;Keywords: carbon-carbon lyase; carboxy-lyase; purine nuclectide biosynthesis
F;3-136/Domain: phosphoribosylaminoimidazole carboxylase catalytic chain homology <PCC>
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                                                                                                                                                                                                                                                                                                                                                                          conserved hypothetical protein - Deinococcus radiodurans (strain R1)
C;Species: Deinococcus radiodurans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C,Species: Listeria monocytogenes
                                                                                                                                                                                                                                                                                                                                    5 HSIVQPPAPPPNAFVEIVSSSTGIIIAVGIFAFIFSFLYKLLQWYNRKSKNK--KRKEQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22 VSSSTGIIIAVGIFAFIFSFL----YKLLQWYNRKSKNKKRKEQIREQIEL-----
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                                                                                                                                                                                                   DB 2; Length 167;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ch 10.8%; Score 78; DB 2; Length 255; Similarity 27.3%; Pred. No. 3.9; 30; Conservative 14; Mismatches 42; Indels
                                                                                                                                                                                                                                                                  28, Indels
                                                                                                                                                                                               11.5%; Score 83; DB 2; Best Local Similarity 33.8%; Pred. No. 0.77; Matches 23; Conservative 15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Superfamily: hypothetical protein H10902
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           160 QKEVENGI 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63 REQIECGL 70
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Best Local Similarity
Matches 30; Conserv
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A;Molecule type: DNA
A;Residues: 1-391 <GLA>
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C, Genetice:
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A;Status; preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1477 <STE>
A;Cross-references: UNIPROT:Q25197; EMBL:M64612; NID:g858746; PID:g858747; PIDN:AAA6820
A;Experimental source: adult polyp
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cross-references: UNIPROT:P2555; EMBL:X59720; NID:g1907116; PIDN:CAA42348.1; PID:e26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RiSteele, R.E.; Mai, N.H.; Lieu, P.; Shenk, M.A. submitted to the EMBL Data Library, May 1995
A; Description: An insulin-like receptor gene is expressed in dividing epithelial cells A; Reference number: 218954
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Oliver, S.G.; Anwar, R.; Brown, A.; Gent, M.E.; Indge, K.J.; James, C.M.; Stateva, submitted to the Protein Sequence Database, March 1992
A;Reference number: S19337
A;Accession: S19338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ::: | |:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | .:: | 
                                                                                    57 KRKEQIREQIELGLLSYGAGVASLPLLNVIAHNPGSVISATPIYKGPCTGVPNSRLLQIT 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19 VEIVSSSTGIIIAVGIFAFIFSFLYKLL -------CMYNRK------SKNK 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C,Species: Hydra vulgaris
C,Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: I18534
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C.Species: Saccharomyces cerevisiae
C.Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 16-Aug-2004
C.Accession: 519338
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2, Length 1477;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F:123-188/Domain: ribonucleoprotein repeat homology <RRM1>F:220-286/Domain: ribonucleoprotein repeat homology <RRM2>F:350-416/Domain: ribonucleoprotein repeat homology <RRM3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Gene: HTK7
C; Superfamily: insulin receptor; protein kinase homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein-tyrosine kinase - Hydra vulgaris
N;Alternate names: insulin-like receptor protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Wap position: 31
C; Superfamily: ribonucleoprotein repeat homology
C; Keywords: nucleus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
10.6%; Score 76; DB
Best Local Similarity 20.9%; Pred. No. 45;
Matches 28; Conservative 25; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Gene: SGD:GBP2
A;Cross-references: SGD:S0000517; MIPS:YCL011c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1042 EKIELIR---ELGOGSFGM---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10.5%;
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                                    29 IIAVGIFAFIFS-
                                                                                                                                                                                                                                         1: | |
276 WIVFA 281
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Best Local Similarity
                                                                                                                                                                                     82 LLNVIA 87
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A; Residues: 1-427 <OLI>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein B0207.12 [imported] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Accession: C87791
R;Anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog
A;Title: Genome sequence of MUID:99065613; PMID:9851916
A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/Projects/C_ele
A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
A;Accession: C87791
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| Experimental Bource: strain A3(2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A,Molecule type: DNA*

A,Residues: 1-654 <STO>

A,Residues: 1-654 <STO>

A,Residues: 1-654 <STO>

A,Residues: 1-654 <STO>

A,Rotces references: GB:chr I; PIDN:AAB52465.1; PID:g1943811; GSPDB:GN00019; CESP:B0207.1

A,Note: Similar to ligand-gated lonic channel

A,Genetics:

A,Genetics: B0207.12

A,Map position: 1
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S;Sesger. K.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream,
submitted to the EMBL Data Library, July 1999
A;Reference number: 221574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ë
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                                                                                                                                                                                                                                                                                                                  61 WILDKEKNIILQNQEALKNPKLLSIISLDKIRDELEFEGRPYA------VKIIAHNEK 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           48 WYNRKSKN-----KKRK-----EQIREQIELGLLSYGAGVASLPLLNVIAHNPG 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         probable integral membrane transport protein - Streptomyces coelicolor C; Species: Streptomyces coelicolor C; Species: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14 PPNAFVEIVSSSTGIIIAVGIFAFIFSFL--YKLLOWYNRKS---KNKKRKEQI----
                                                                                                                                                                                             Gape
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ω
                                                                                                                                                                                                                                                                                                                                                                                                                      92 SVISATPIYKGPCTGVPNSRLLQITSGTAEENTRILNHDGRNPDGSINV 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 654;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26; Indels
                                                                                                            ch 10.8%; Score 77.5; DB 2; Length 3:
1 Similarity 28.4%; Pred. No. 6;
31; Conservative 14; Mismatches 31; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2;
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A;Molecule type: DNA
A;Residues: 1-298 <SEE>
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29.9%; Pred. No. 13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 29.9<sup>5</sup>
Matches 26; Conservative
                                                                                                            Query Match
Best Local Similarity
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                                    A, Gene: Cj0793
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C,Genetics:
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Cross-references: UNIPROT:Q99RV2; GB:BA000018; PID:g13702121; PIDN:BAB43413.1; GSPDB:<
Experimental source: strain N315
o, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasud DNA Res. 3, 109-136, 1996
A; Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocysti
                                                                                                                                                                                                                                                                                           A/Residues: 1-399 -KANNA/Cross-references: UNIPROT:P74550; EMBL:D90916; GB:AB001339; NID:g1653715; PIDN:BAA186 A/Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996 C/Genetics:
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A/Reference number: Z21614
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R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, C.; Sekimizu, C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K. Lancet 357, 1225-1240, 2001
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A,Reference number: A89758; MUID:21311952; PMID:11418146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /pothetical protein SA2112 [imported] - Staphylococcus aureus (strain N315)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Species: Staphylococcus aureus
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C;Accession: D90031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12 APPPNAFVEIVS--SSTGIIIAVG-----IFAFIFSFLYKLLQWYNRKSKNKKKK
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C.Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C.Accession: T36781
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Accession: S76745
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1; Length 399;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 QIREQIELGLLSYGAGVASLPLLN-VIAHNPGSVISATPIY 100
                                                                                                                                                                     A, Reference number: S74322; MUID: 97061201; PMID: 8905231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10.4%; Score 75; DB 1
23.8%; Pred. No. 13;
iive 23; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Superfamily: chromate resistance protein A
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Best Local Similarity 23.8*
Matches 24, Conservative
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A,Molecule type: DNA
A,Residues: 1-305 <KUR>
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Residues: 1-1220 <CHU>
Cross-references: UNIPROT:P39928; GB:Z47047; EMBL:Z38059; NID:g603997; PID:g763199; MI
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C;Accession: 876745
R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asemizu, B.; Nakamura, Y.; Miyajima, N.
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C.Species: Saccharomyces cerevisiae
C.Date: 02-Dec-1994 #sequence_revision 02-Dec-1994 #text_change 09-Jul-2004
C.Accession: S48387; S48888
R.Churcher, C.
                                                                                                                                                    189 RKLMVRODNPPPRAAKEFSKKATREBIDNGFEVPIINLPY8-MWQSLKDMFKECGHVLR
                                                                            4 RHSIVQPPAPPPNAFVEIVSSSTGIIIAVGIFAFIFSFLYKLLQWYNRKSKNKKRKEQIR
                                                                                                                                                                                                                                        64 BQIELGLLSYGAGVASLPLLNVIAHNPGSVISATPIYKGPCTGVPNSRLLQITSGTAEEN
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            Gaps
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ence 262, 566-569, 1993
litle: A yeast protein similar to bacterial two-component regulators
eference number: 8488888; MUID:94024010; PMID:8211183
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F:334-350/Domain: transmembrane #status predicted <TM2>
F:1090-1206/Domain: response regulator homology <RRH>
F:1144/Binding site: phosphate (Asp) (covalent) #status predicted
18; Mismatches 74; Indels
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31, Conservative
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A,Residues: 1-359 <OLI>
A,Crose-references: UNIPROT:Q8CK22; EMBL:AL096811; PIDN:CAB46778.1; GSPDB:GN00070; SCOED
A,Experimental source: strain A3(2)
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C, Superfamily: D-serine permease
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Accession: S05654
Cummings, D.J.; Domenico, J.M.
Mol. Bidl. 204, 815-839, 1989, 1980
Accession: Solorico, J.M.
Accession: Solorico, J.M.
Accession: Soloffs
Accession: Soloffs
Molecule type: DNA
Residues: 1-433 <CUM>
Residues: 1-433 <CUM>
Residues: Teferences: UNIPROT: P15563

33 intron protein - Podospora anserina mitochondrion Species: mitochondrion Podospora anserina Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 09-Jul-2004

ENTRILMHDGRNPDGSIN 139
::: : | | | | |
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Search completed: November 15, 2004, 14:58:22 Job time : 45 seca

22 VSSSTGIIIAVGIFAFIFSFLY------KLLOWYNRKSKNKKKKK---EQIREQ 65

20; Mismatches

Query Match
Best Local Similarity 23.93
Matches 33; Conservative

8 8 8

A, Genome: mitochondrion A, Genetic code: SGC3 C, Keywords: mitochondrion 28;

DB 2; Length 433; 18; nes 57; Indels

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

November 15, 2004, 14:32:21; Search time 195 Seconds (without alignments) 413.089 Million cell updates/sec

US-09-943-002-14
720
1 MGRHSIVQPPAPPPNAFVE.....EENTRILAHDGRNPDGSINV 140 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1825181 segs, 575374646 residues Searched:

1825181 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

UniProt_02:*
1: uniprot_sprot:*
2: uniprot_trembl:* Датараве :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	•	-						Q8dgc1 synechococc		Q22040 caenorhabdi						Q899q9 clostridium	_		-	_				Q95q97 caenorhabdi	Q833i4 enterococcu	Q9ffw5 arabidopsis	Q8rf10 fusobacteri	Q6yt74 oryza sativ	Bac84718 oryza sat	Q9x9y6 streptomyce	Q8tq34 methanosarc
SUMMAKIES	дв пр	2 Q918V6	2 Q7QРН4			2 Q99SX9	-	2 Q7A4Q3	2 Q8DGC1	1 PUR6_AQUAE				2 Q6F2A9	2 Q8C115	2 Q8LP72	2 Q899Q9	2 Q9RWX1	2 Q8Y5M5	2 Q71XY1	2 AAT04834	2 Q929Y5	2 Q9PPC6				2 Q9FFW5		_	2 BAC84718	2 Q9X9Y6	2 Q8TQ34
	Length	140	908	431	431	. 431	431	431	574	167	636	734	431	443	1491	633	664	255	391	391	391	392	339	430	430	172	681	187	280	280	298	308
ي و و	Match	100.0	11.9	11.7	11.7	11.7	11.7	11.7	11.7	11.5	11.5	11.4	11.2	11.0	11.0	11.0	11.0	10.8	10.8	10.8	10.8	10.8			。	•		10.6	•	10.6	•	10.6
	Score	720	85.5		84	84	84	84	84	m	82.5	82	80.5	79.5	79.5	79	79	78	78	78	78	7	77.5	77.5	77.5	77	76.5	92	92	92	96	92
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				P39928 saccharomyc		Q7rg91 plasmodium		Aas43502 bacillus	Q821z3 chlamydophi	O8pz47 methanosarc	Q9y438 homo sapien	Q6g6z9 staphylococ		Q99rv2 staphylococ	
	Q7M857	HTK7 HYDAT	GBP2_YEAST	SLN1_YEAST	P74550	Q7RG91	Q72ZR7	AAS43502	LPXB CHLCV	Q8PZ47	Q9Y438	066629	Q8NV71	Q99RV2	
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	765	1477	427	1220	399	481	508	508	626	848	892	305	305	305	
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ALIGNMENTS

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PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=MRSA252;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           74 GAGVASLPLLNVIAHNPGSVISATPIYKGPCTGV------PNSRLLQ-----ITSGT 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         441 GHGVLATPVLTL----SSIIGSGSI---RWTGVSISNDITSANSNRLEAGTNGDMTPGS 492
                                                                                                                                                                                                                                                                                                                                                                                                            PPNAFVEIVSSSTGIIIAVGIFAFIFSFLYKLLQWYNRKSKNKKRKEQIREGILSY 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Holden M.T.G., Feil B.J., Lindsay J.A., Peacock S.J., Day N.P.J., Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A., Bason N., Bentley S.D., Chillingworth T., Churcher C., Clark L., Corton C., Cronin A., Doggett J., Dowd L., Feltwell T., Hance Z., Harris B., Hauser H., Holroyd S., Jagels K., James K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K., Ormond D., Quail M.A., Rabbinowitsch B., Rutherford K., Sanders M., Sharp S., Simmonds M., Stevens K., Whitehead S., Barrell B.G., Earkhill J., "Complete genomes of two clinical Staphylococcus aureus strains: evidence for the rapid evolution of virulence and drug resistance."; Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                      preliminary data.

EMBL; ARCENIONOISF, EAA36911.1; -.
GO; GO:0003677; F:DNA binding; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
InterPro; IPRO01965; Znf PHD.
PERM; PPF00628; PHD; 1.
SEQUENCE 806 AA; 90537 MW; CD93E0653EF38DB9 CRC64;
                                             Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                / Match 11.9%; Score 85.5; DB 2; Length 806; Local Similarity 24.5%; Pred. No. 18; hs. Conservative 21; Mismatches 44; Indels 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Adenylosuccinate lyase (EC 4.3.2.2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Staphylococcus aureus subsp. aureus MSSA476.
Bacteria; Firmicutes; Bacillales; Staphylococcus.
NCBI TaxID=282459;
Olsen G.J., Sogin M.L.;
"Draft sequence of the Giardia lamblia genome.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; BX571857; CAG43636.1; ...
InterPro; IPR003031; D_crystallin.
InterPro; IPR000362; Fumarate_lyase.
InterPro; IPR00848; L-Aspartase-like.
InterPro; IPR00448; L-Aspartase-like.
Pfem; PF00206; Lyase_1; I.
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PROSITE; PS00163; FUMARATE_LYASES; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         493 ASAANGPHASMRQTNSIKNTKVI 515
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  Olsen G.J.,
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----TFANIPPE 193
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Buright M.C., Foster T.J., Moore C.B., Hurst L., Atkin R., Barron A.,
Benright M.C., Calark L., Chillingworth C., Chillingworth T.,
Churcher C., Clark L., Corton C., Cronin A., Dogget J., Dowd L.,
Churcher C., Clark L., Corton C., Cronin A., Dogget J., Dowd L.,
A Feltwell T., Hance Z., Harris B., Hauser H., Holroyd S., Jagels K.,
A James K.D., Lemnard N., Line A., Mayes R., Moule S., Mungall K.,
Cormond D., Quail M.A., Rabbinowitsch E., Rutherford K., Sanders M.,
Sharp S., Simmonds M., Stevens K., Whitchead S., Barrell B.G.,
Spratt B.G., Parkhill J.,
Complete genomes of two clinical Staphylococcus aureus strains:
evidence for the rapid evolution of virulence and drug resistance.",
proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
R EMBL, BX571856, GAG409851.;
R InterPro; IPR003031; D. Crystallin.
R InterPro; IPR003031; D. Crystallin.
R InterPro; IPR0030848; Limarate_lyase.
R InterPro; IPR00848; Limarate_lyase.
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33 GIFAFIFSFLYKLLOWYNRKSKNKKRKEQIREQIBLGLLSYGAGVASLPLLNVIAHNPGS 92
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Best Local Similarity 26.5%; Pred. No. 12;
Matches 26; Conservative 15; Mismatches 35; Indels
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                                     93 VISATPIYKGPCTGVPNSRLLQITSGTAEENTRILNHD 130
                                                                                                                                  93 VISATPIYKGPCTGVPNSRLLQITSGTAEENTRILNHD 130
                                                                                                                                                                        ----IĞTAPVSTQTLQRD 217
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Last annotation update)
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Adenylosuccinate lyase.
Name-purs, OrderedLocusNames-SAV1908,
Staphylococcus aureus (strain Muso / ATCC 700699)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Staphylococcus aureus subsp. aureus MRSA252.
Bacteria, Firmicutes; Bacillales; Staphylococcus
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PROSITE; PS00163; FUMARATE_LYASES; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
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05-JUL-2004 (TrEMBLrel. 27, Last sen
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05-JUL-2004 (TrEMBLrel. 27, Last an
Adenylosuccinate lyase (EC 4.3.2.2)
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                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR004769; Pur lyase.
Pfam; PF00206; Lyase 1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PR00145; DCRYSTALLIN.
PRINTS; PR00149; FUMRATELYASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Name=purB; ORFNames=SAR2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               194 IESYVCKHLG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (TrEMBLrel. 17, (TrEMBLrel. 17,
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HSSP;

OC SWR RAPARA BRANCO SWR BRANCO S

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142 GVHAEPTTFGVKWALWYTEMORNLORFKOVREBIBVGKWSGAVG------TPANIPPE 193
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              33 GIFAFIFSFLYKLLOWYNRKSKNKKRKEQIREQIBLGLLSYGAGVASLPLLNVIAHNPGS 92
                                                                                                                                                                                                                                                                                                                                         22; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDINE-21311952; PubMed=11418146; Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I., Curoda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I., Cui L., Gquchi A., Aoki K.-I., Nagai Y., Lian J.-O., Ito T., Kanamori M., Matuyama A., Murakami H., Hosoyama A., Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C., Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J., Kanahisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.; Whole genome sequencing of meticillin-resistant Staphylococcus
                                                                                                                                                                                                                                                                      Query Match 11.7%; Score 84; DB 2; Length 431; Best Local Similarity 26.5%; Pred. No. 12; Matches 26; Conservative 15; Mismatches 35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11.7%; Score 84; DB 2; Length 431; 26.5%; Pred. No. 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15; Mismatches 35; Indels
                                                                                                                   TIGRPAMS; TIGRO0928; purB; 1.
PROSITE; PSO0163; FUMARATE_LYASES; 1.
COMPLETE protecome; Lyase.
SEQUENCE 431 AA; 49603 MW; 493F79CBE814B9E5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           431 AA; 49603 MW; 493F79CBE814B9E5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             93 VISATPIYKGPCTGVPNSRLLQITSGTAEENTRILNHD 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      194 IESYVCKHLG-----IGTAPVSTOTLORD 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           93 VISATPIYKGPCTGVPNSRLLQITSGTAEENTRILNHD 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Name=purB; OrderediccusNames=SA1724;
Staphylococcus aureus (strain N315).
Bacteria; Firmicutes; Bacillales; Staphylococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             431 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lancet 357:1225-1240(2001).
EMBL, AP003135; BAB42994.1; -...
EMBL, AP003135; BAB42994.1; -...
InterPro; IPR003031; D_crystallin.
InterPro; IPR003031; D_crystallin.
InterPro; IPR003052; Funarate lyase.
InterPro; IPR003052; Funarate lyase.
InterPro; IPR00494; L-Aspartase-like.
Pfam; PR00145; DGR\(\frac{T}{2}\) DGR\(\frac{T}{2}\) DGR\(\frac{T}{2}\) TIT\(\frac{T}{2}\) DGR\(\frac{T}{2}\) TIT\(\frac{T}{2}\) DGR\(\frac{T}{2}\) TIT\(\frac{T}{2}\) DGR\(\frac{T}{2}\) TIT\(\frac{T}{2}\) TIT\(\frac{T}{2}\) TURATELIAN.
PRINTS; PR00149; PUMRATELYASE.
TIGREAMS; TIGR00928; PURE; 1
PR053TE; PS00163; FUMRATELYASES; 1.
COMPLETE PS01063; FUMRATELYASES; 1.
InterPro; IPR004769; Pur lyase.
                                Pfam; PF00206; Lyase 1; T. PRINTS; PR00145; DCRYSTALLIN. PRINTS; PR00149; FUMRATELYASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 26.5$
Matches 26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Adenylosuccinate lyase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=158879;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 aureus."
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07A403
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    33 GIPAFIBSFLYKLLQWYNRKSKONKRKEQIREQIELGLLSYGAGVASLPLLNVIAHNPGS 92
                                                                            SEQUENCE FROM N.A.

SERAIISMUSO / ATCC 700699;

MEDLINE-21311952; PubMed=11418146;

Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,

Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-O., Ito T.,

Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,

Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,

Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,

Kanehisa M., Yamashita A., Oshima K., Puruya K., Yoshino C., Shiba T.,

Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.,

"Whole genome sequencing of meticillin-resistant Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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BEDLINE-22040171; PubMed=12044378;
BADA T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A., Nagai Y., Iwama N., Asano K., Naimi T., Kuroda H., Cui L., Yamamoto K., Hiramatsu K.;
"Genome and virulence determinants of high virulence community-acquired MRSA.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GO; GO: 0004019; Fiadenylosuccinate lyase activity; IEA. GO; GO: 0016829; F: lyase activity; IEA. GO; GO: 0016829; F: lyase activity; IEA. GO; GO: 0009152; F: purine ribonucleotide biosynthesis; IEA. InterPro; IPR003031; D_crystallin.
InterPro; IPR003031; P_marate lyase.
InterPro; IPR00848; L-Aspartäse-like.
InterPro; IPR00499; Purlyase.
PEMINTS; PR00145; DCRYSTALLIN.
PRINTS; PR00149; FUWRATELYASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11.7%; Score 84; DB 2; Length 431; 26.5%; Pred. No. 12; Live 15; Mismatches 35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             49603 MW; 493F79CBE814B9E5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             93 VISATPIYKGPCTGVPNSRLLQITSGTAEENTRILNHD 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----IGTAPVSTOTLORD 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    05-JUL-2004 (TrEMBLrel. 27, Created).
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Bacteria; Firmicutes; Bacillales; Staphylococcus.
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Bacteria, Firmicutes, Bacillales, Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    431 AA
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EMBL, AP004828; BAB95714.1; -

GO; GO:0016829; F:lyase activity; IEA.

Interpro; IPR003031; D_crystallin.

Interpro; IPR000362; Fumarate lyase.

Interpro; IPR008948; L-Aspartase-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TIGRFAMS; TIGR00928; purB; 1.
PROSTIE; PSO1163; FUMARATE_LYASE8; 1.
COMPLETE protecome; Lyase.
SEQUENCE 431 AA; 49603 MW; 493F790
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lancet 357:1225-1240(2001).
EMBL; AP003363; BABS8070.1; -.
PIR; C89979; C89979.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
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                            NCBI_TaxID=158878;
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RESULT 6 Q7A0G9

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"The complete genome of the hyperthermophilic bacterium Aquifex
                                                                   Nature 392:353-358(1998)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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Q22040;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nakamura Y., Kaneko T., Sato S., Ikeuchi M., Katoh H., Sasamoto S., Watanabe A., Iriguchi M., Kawashima K., Kimura T., Kishida Y., Kiyokawa C., Kobara M., Matsumoto M., Matsumo A., Nakazaki N., Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S., Sugimoto M., Takeuchi C., Yamada M., Tabata S., 17 Complete genome structure of the thermophilic cyanobacterium Thermosynechococcus elongatus BP-1.";

Thermosynechococcus elongatus BP-1.";

DNA Res. 9:123-130(2002)

I. FUNCTION: Part of a binding-protein-dependent transport system.

Probably responsible for the translocation of the substrate across
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        34 IFAFIFSFLYKLLQWYNRKSKNKKRKEQIREQIELGLLSYGAGVASLPLLNVIAHNPGSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27; Indels 16; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Thomatry responsible to the transfordation of the substrate and the membrane (By similarity).
-!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
-!- SUBCELLULAR. ECATION: Integral membrane protein (By similarity).
-!- SIMILARITY: Belongs to the binding-protein-dependent transport BYSTER protein permease family.

EMBL; APOGS177; BAC0949:1; -.
GO; GO:0005215; Firansporter activity; IEA.
GO; GO:0005215; Firansporter activity; IEA.
InterPro; IRPRO005215; BPD transp.
InterPro; IRPRO005215; BPD transp.
Pfam; PRO0528; BPD transp.
PROSITE; PSS50928; ABC_TMI; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIINB=98196666; PubMed=9537320; DOI=10.1038/32831; Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L., Graham D.E., Overbeek R., Snead M.A., Keller M., Aujay M., Huber R., Feldman R.A., Short J.M., Olsen G.J., Swanson R.V.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ch 11.7%; Score 84; DB 2; Length 574; I Similarity 27.6%; Pred. No. 17; 24; Conservative 20; Mismatches 27; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-DEC-1998 (Rel. 37, Last sequence update).
01-OCT-2004 (Rel. 45, Last annotation update)
Phosphoribosylaminolmidazole carboxylase catalytic subunit
(BC 4.1.1.21) (AIR carboxylase) (AIRC).
Name=purE; OrderedLocusNames=AQ_1178;
                                                                                                                                                                                                                                                                                                                              Synechococcus elongatus (Thermosynechococcus elongatus). Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria, Aquificae, Aquificales, Aquificaceae, Aquifex.
NCBL_TaxID=63363;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Complete proteome, Transmembrane, Transport.
SEQUENCE 574 AA; 64027 MW; 3A478A3F80FB4BBD CRC64;
                                                                                                                                                                                                    Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            167 AA
                                                                                                     574 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94 ISATPIYKGPCTGVPNSRLLQITSGTA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          :: :: | | : : | | | 118 LALIALFPGSRMGVELAAIILIYTGMA 144
                                                                                                                                                                         Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=22225144; PubMed=12240834;
                                                                                                                                                                                                                                                                        transporter permease protein.
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                                                                                                                                                                                                    01-MAR-2003 (TrEMBLrel. 23, 01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                      OrderedLocusNames=t112397;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=32046;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Aquifex aeolicus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PUR6_AQUAE
067239;
                                                                                                                                                                      01-MAR-2003
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OBDGC1
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its tuse by non-profit institutions as long as its concent is in no way
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100 YSIVQMPAGIPVATVAIGNATNAGLLAVRILSIKYPBYAKKLDBYTEKLKBKVAKMNBBL 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5 HSIVQPPAPPPNAFVEIVSSSTGIIIAVGIFAFIFSFLYKLLQWYNRKSKNK--KRKEQI 62
FUNCTION: This subunit can alone transform AIR to CAIR, but in association with purK, which possesses an ArPase activity, an enzyme complex is produced which is capable of converting AIR to CATALYTIC ACTIVITY: 5-amino-1-(5-phospho-D-ribosyl)imidazole-4-carboxylate = 5-amino-1-(5-phospho-D-ribosyl)imidazole + CO(2). PATHWAY: De novo purine biosynthesis; sixth step.
SUBUNIT: Homocctamer [By similarity).
SIMILARITY: TO OTHER BACTERIAL PURE, ALSO TO AIR CARBOXYLASE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Complete proteome, Decarboxylase, Lyase, Purine biosynthesis. SEQUENCE 167 AA, 18037 MW, 99A62BE6000F50F4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1; Length 167;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 33.8%; Pred. No. 5;
Matches 23; Conservative 15; Mismatches 28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Minx M.;
Submitted (DEC-1995) to the BMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-WAR-2004 (TrEMBLrel. 26, Last Sequence update) 01-WAR-2004 (TrEMBLrel. 26, Last annotation update) Hypothetical protein SSSD1.1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11.5%; Score 83; 33.8%; Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HSSP, Q9WYS7; 104V.
InterPro; IPR000031; AIR_carboxyl.
Pfam; PF00731; AIRC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ProDom; PD002193; AIR_carboxyl; 1.
TIGRFAMB; TIGR01162; purE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=99069613; PubMed=9851916;
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Science 282:2012-2018(1998).
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666 ------ASTSAPPPPPVSVVAAHPPMGSAGVVSVAASPSTNGPLSSLPNT-- 710
                                                                                                                                                                                                                                    58 RKEQIREQIBLGLLSYGAGVASLPLLNVIAHNP-GSV----ISATPIYKGPCTGVPNSRL 112
                                                                                                                                                              8 VOPPAPPPNAFVEIVSSST-----GIIIAVGIFAFIFSFLYKLLQWYNRKSKONKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Zhang Y.-Q., Ren S.-X., Li H.-L., Wang Y.-X., Fu G., Yang J.,
Qin Z.-Q., Miao Y.-G., Wang W.-Y., Chen R.-S., Shen Y., Chen Z.,
Yuan Z.-H., Zhao G.-P., Qu D., Danchin A., Wen Y.-M.;
"Genome-based analysis of virulence genes in a non-biofilm-forming staphylococcus epidermidis strain (ATCC 12228).";
Mol. Microbiol. 49:1577-1593 (2003)
HSSP; Q9X010, 1C3C.
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11.2%; Score 80.5; DB 2; Length 431;
Best Local Similarity 34.0%; Pred. No. 27;
Matches 17; Conservative 13; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 33 GIFAFIFSFLYKLLQWYNRKSKNKKRKEQIREQIELGLLSYGAGV-ASLP
                   11.4%; Score 82; DB 2; Length 734; 26.9%; Pred. No. 35; tive 15; Mismatches 36; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GO; GO:0004018; F:adenylosuccinate lyase activity; IEA.
GO; GO:0016829; F:lyase activity; IEA.
GO; GO:0009152; P:purine ribonucleotide biosynthesis; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  49591 MW; 08D770CAB109B72A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Adenyloguccinate lyase.
OrderedLocusNamns=SRIS3;
Staphylococcus epidermidis.
Bacteria; Firmicutes; Bacillales; Staphylococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        431 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           443 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR003031; D_crystallin.
InterPro; IPR00362; Fumarate_lyase.
InterPro; IPR008948; L-Aspartase-like.
InterPro; IPR004769; Pur_lyase.
Dfan, Df00706; Lvase 1: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IGRFAMS; TIGR00928; purB; 1.
ROSITE; PS00163; FUMARATE LYASES; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PR00145; DCRYSTALLIN.
PRINTS; PR00149; FUMRATELYASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (TrEMBLrel. 23, 1
(TrEMBLrel. 23, 1
(TrEMBLrel. 26, 1
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                           Query Match
Best Local Similarity 26.9
Matches 35, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Complete proteome; Lyase. SEQUENCE 431 AA; 49591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                113 LOITSGTAEE 122
                                                                                                                                                                                                                                                                                                                                                                                                     711 IOKTHATDDE 720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN=ATCC 12228;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=ATCC.12228
PubMed=12950922;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=1282;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    O6F2A9;
01-OCT-2004 (
01-OCT-2004 (
01-OCT-2004 (
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Q6F2A9
ID Q6F2A
AC Q6F2A
DT 01-OC
DT 01-OC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DBCRT6
                                                                                                                                                                                                                                                                                           셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               469 PPSEPSNALRYGIADNVDLPIFMLAAVFGLLFCFACGLFAWRCFHNKNKKSKRKKSRSNS 528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62 --IREQIELGLLSYGAGVASLPLLNVIAHNPGSVISATPIYKGPCTGVPNSRLLQITSGT 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      529 TPSKTYODYGRFTYGDGSSS-----SOPG----TETYY----EPSLRLLD---- 565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PPAPPNAPVEIVSSSTG--IIIAVGIFAFIFSFLYKLLQW---YNRKSKNKKRKEQ--- 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Anopheles gambiae str. PEST.
Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Nematocera, Culicoidea, Anopheles.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Anopheles Genome Sequencing Consortium,
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        43; Indels 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 636;
                           Waterston R.;
Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                    Wilson R.; Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            71728 MW; 2894A1E7428C0793 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     734 AA; 80917 MW; A409AFD311EAB054 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAR-2004 (TrEMBLrel. 26, Created)
01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AgCP5939 (Fragment).
Name=agCG54493; ORFNames=ENSANGG0000008214;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     734 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ch 11.5%; Score 82.5; D
1 Similarity 23.7%; Pred. No. 27;
32; Conservative 19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
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EMBL, AAAB01008960; EAA11826.1; -.
InterPro; IPR001611; LRR.
InterPro; IPR007092; LRR.
InterPro; IPR003591; LRR. typ.
Pfam; PP00560; LRR; 10.
PRINTS; PR00019; LEURICHRPT.
                                                                                                                                                                                                                                                             HSSP; PS6276; 1FHG.
WormPep; SSD1.1; CE29458.
InterPro; 1PR001361; PN_III.
InterPro; IPR001359; IG.
InterPro; IPR007110; IG-11ke.
InterPro; IPR001598; IG_C2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE, PS50853; FN3; 1.
PROSITE; PS50835; IG LIKE; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ------DHEWRGP 572
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                                                                                                                                                                                                             EMBL; U41530; AAA83273.3;
PIR; T16774; T16774.
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                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PP00041; fn3; 1.
Pfam; PP00047; ig; 3.
SMART; SM00060; FN3; 1.
SMART; SM00409; ig; 3.
SMART; SM00409; igc; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   al protein.
636 AA; 7
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Best Local Similarity
                                                                                                         SEQUENCE FROM N.A. STRAIN-Bristol N2;
STRAIN-Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=180454;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical
SEQUENCE 63
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SEQUENCE
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Q7Q696
RANGE STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND 
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Gaps

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69 GLLSYGAGVASLPLLNVIAHNPGSVISATPIY---KGPCTGVPNSRLLQITSGTAEB--- 122
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Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
Adachi J., Aizawa K., Akimura T., Hara A., Hashizume W.,
Adachi J., Aizawa K., Akimura T., Hara A., Hashizume W.,
Hayashida K., Hayatsu N., Haramoto K., Hiraoka T., Hirozane T.,
Aktoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
Tagawa A., Takahashi F., Takaku-Akahira S., Takada Y., Tanaka T.,
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.

HSSP: 008967; 1FHW.
                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN-C57BL/6J; TISSUE=Head;
MEDLINE=20499374; PubMed=11042159;
MEDLINE=20499374; PubMed=11042159;
Carninol P., Shibata Y., Hayatan N., Sugahara Y., Shibata K., Itoh M.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
"Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
Genome Res. 10:1617-1630(2000).
      the RIKEN Genome Exploration Research Group Phase I & II Team; "Analysis of the mouse transcriptome based on functional annotation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9 QPPAPPPNAFVEIVSSSTGIIIAVGIFAFIFSFLYKLLQWYNRKSKNKKKKEQIREQIEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=CSTBL/GJ. TISSUB=Head;
MEDLINE=CSTBL/GJ. TISSUB=Head;
MEDLINE=CSTBL/GJ. PubMed=11076861;
MEDLINE=20530913; PubMed=11076861;
MEDLINE=20530913; PubMed=11076861;
MEDLINE=20530913; PubMed=11076861;
Mishix R., Itoh M., Itoh M., Sumin N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watshiwagi K., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J. Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J. WRIKEN Integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11.0%; Score 79.5; DB 2; Length 1491; 27.2%; Pred. No. 1.4e+02; tive 22; Mismatches 42; Indels 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1491 AA; 167749 MW; 1326DCD4F5E33018 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MGD; MGI:2146813; AI256725.
GO; GO:0005856; C:cytoskeleton; IEA.
GO; GO:0003779; F:actin binding; IEA.
GO; GO:0003774; F:arp binding; IEA.
GO; GO:000774; F:motor activity; IEA.
InterPro; IPR000029; Band_4.1.
InterPro; IPR0000857; MYTH4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001849; PH.
InterPro; IPR011036; PH related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS50057; FERM 3; 1.
PROSITE; PS50003; PH_DOMAIN; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SMART; SM00295; B41; 1.
SMART; SM00139; MYTH4; 1.
SMART; SM00233; PH; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 27.2 tes 37, Conservative
                                                                  60,770 full-length cDNAs
Nature 420:563-573(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00784; MyTH4; 1.
Pfam; PF00169; PH; 1.
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Matches
         RATER SEE STANDER 
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Mus musculus 0 day neonate head cDNA, RIKEN full-length enriched
Ilbrary, clone:4831441H15 product:hypothetical Scrine-rich region/Band
4.1 family/PH domain profile/Core domain in kinesin and myosin
motors/Pleckstrin homology (PH) domain containing protein, full insert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PVEIVSSSTGIIIAVGIFAFIFSFLYKLL------QWYNRKSKNKKRKEQIREQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=C57BL/6J; TISSUE=Head; MEDIJUR=2108566), PubMed=11217851; RIKEN FANTOM CONSOCTIUM; CONSOCTIUM; "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                   Birren B.W., Stange-Thomann N., Hafez N., DeCaprio D., Fisher Butler J., Blkins T., Kodira C.D., Major J., Wang S., Nicol R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 443;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN-L1;
Knight T. Jr., Fournier G.;
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AE017263; AAT75357.1; -.
SEQUENCE 443 AA; 50263 MW; F0B9AF49504EBE19 CRC64;
                                                                                                                                                                                                                                                                                                                                                     Nusbaum C.,
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases
                                                                                            Bacteria, Firmicutes, Mollicutes, Entomoplasmatales,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=C57BL/60; TISSUE=Head;
MEDLINE=9279233; PubMed=10349636;
Carninci P., Hayashizari Y.;
"High-efficiency full-length cDNA cloning.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT; 1491 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11.0%; Score 79.5; D
24.8%; Pred. No. 35;
:ive 26; Mismatches
Chromosomal replication initiator protein. ORFNames=Mf1001;
                                                                                                                                 Entomoplasmataceae; Mesoplasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Meth. Enzymol. 303:19-44(1999)
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STRAIN=C57BL/6J; TISSUE=Head;
The FANTOM CONSORTium,
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                                                           Mesoplasma florum L1
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tes 31; Conserv
                                                                                                                                                               NCBI_TaxID=265311;
                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                        STRAIN=L1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Receptor-like procein kinase.
Nicotiana tabacum (Common tobacco).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamiids; Solanales; Solanaceae; Nicotiana.
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MEDLINE-21914716; PubMed=11917080;

MEDLINE-21914716; PubMed=11917080;

MEDLINE-21914716; PubMed=11917080;

MEDLINE-21914716; PubMed=11917080;

Troopy engine of a temperature-sensitive leucine-rich repeat receptor-like protein kinase gene by hypersensitive cell death and if the protein kinase gene by hypersensitive cell death and if the plant cell physiol. 43:266-274(2002).

MEDLINELARITY: Belongs to the Ser/Thr protein kinase family.

MEDLINELARITY: Belongs to the Ser/Thr protein kinase family.

MEDLINELARITY: Protein serine/threonine kinase activity; IEA.

MEDLINELARITY: Princeptor activity; IEA.

MEDLINELARITY: Princeptor activity; IEA.

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MEDLINELARITY: PRINCEPTO: PROTECTOR ACTIVITY; IEA.
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PROSITE; PSSO011; PROTEIN KINASE_OM; 1.
PROSITE; PSO0108; PROTEIN KINASE_ST; 1.
ATP-binding; Kinase; Receptor; Sērine/threonine-protein kinase;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-2002 (TrEMBLrel. 22, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                          633 AA
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nterPro; IPR000719; Prot kinase.
nterPro; IPR008271; Ser thr pkin AS.
(Em; PF000560; LRR; 6.
fam; PF00069; Pkinase; 1.
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579 -ILSYSA--ASL-YTSLIYKN--
                                                                                                                --NTRILNHDGRNPDG 136
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Search completed: November 15, 2004, 14:57:34 Job time : 198 secs